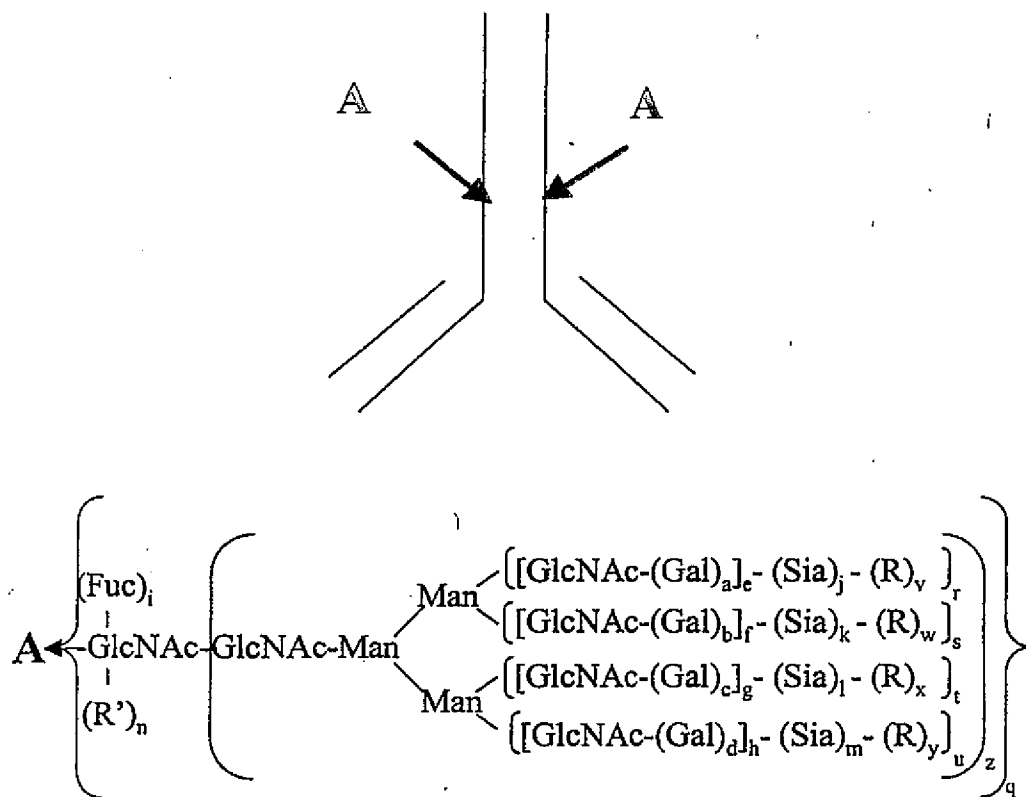


226/497



a-d, i, l, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

$$j-k \text{ (independently selected)} = 0 \text{ or } 1.$$

M = 0 to 20.

$$n, v-y = 0; z = 0 \text{ or } 1;$$

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 49A

227/497

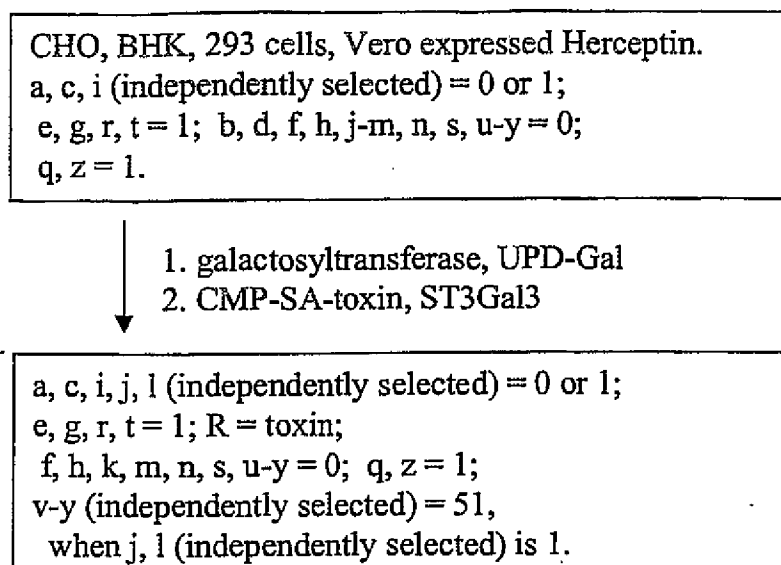


FIG. 49B

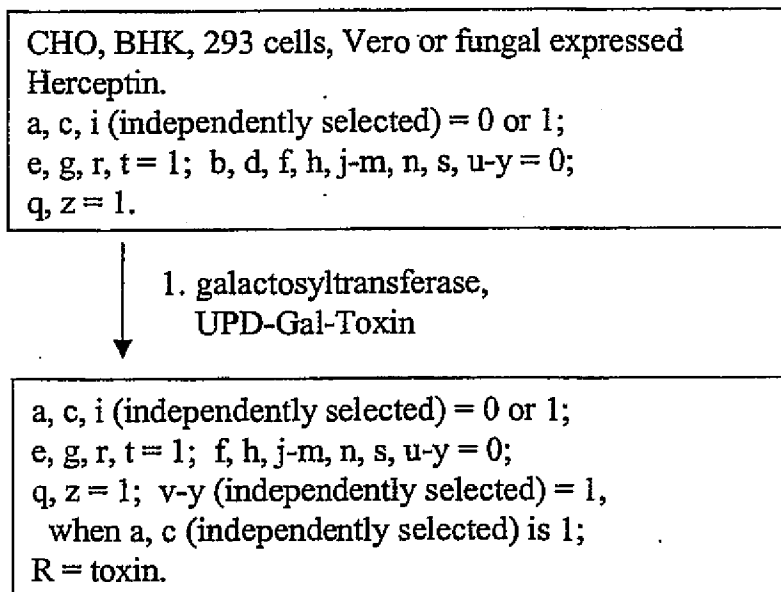


FIG. 49C

228/497

Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

2. Galactosyltransferase, UDP-Gal

↓ 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D



230/497

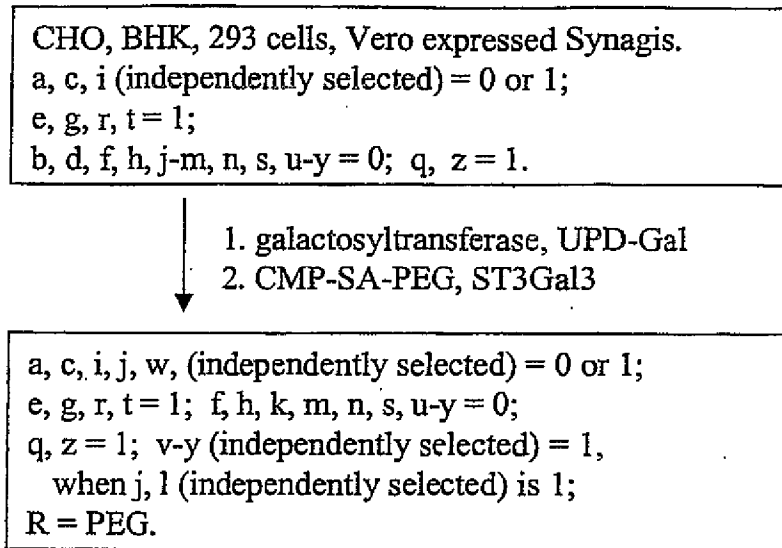


FIG. 50B

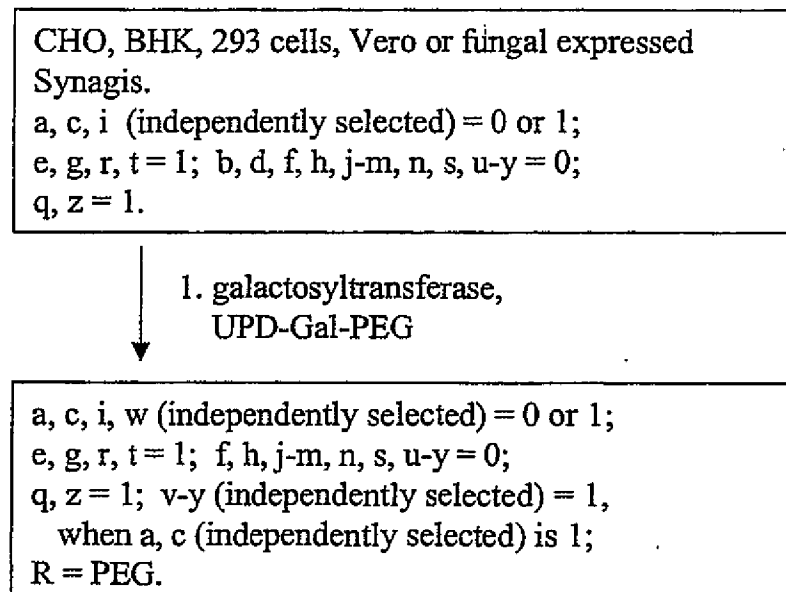


FIG. 50C

231/497

Fungi expressed Synagis.

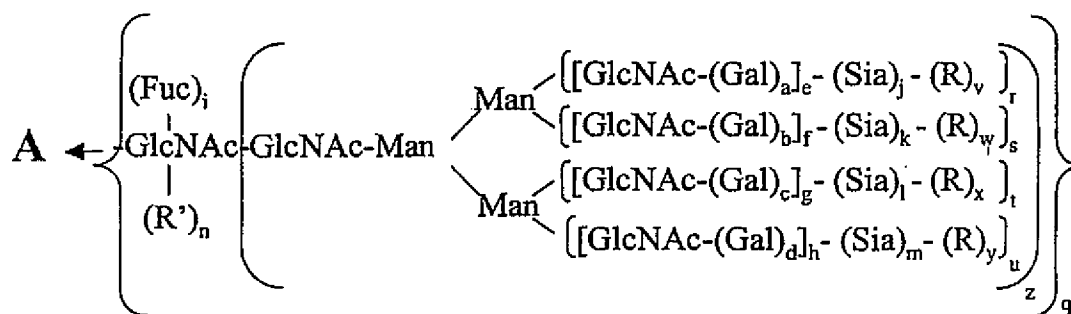
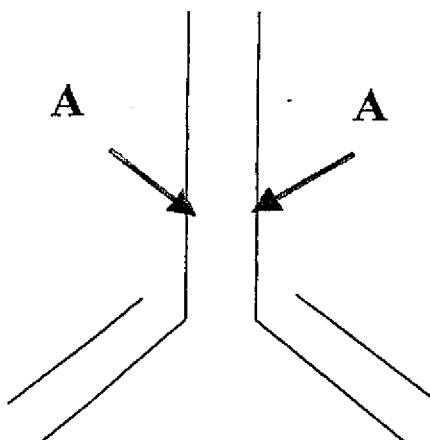
e, g, i, r, t (independently selected) = 0 or 1;  
a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓  
1. Endo-H  
2. Galactosyltransferase, UDP-Gal  
3. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 50D

232/497



a-d, i, q-u, w (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 51A

233/497

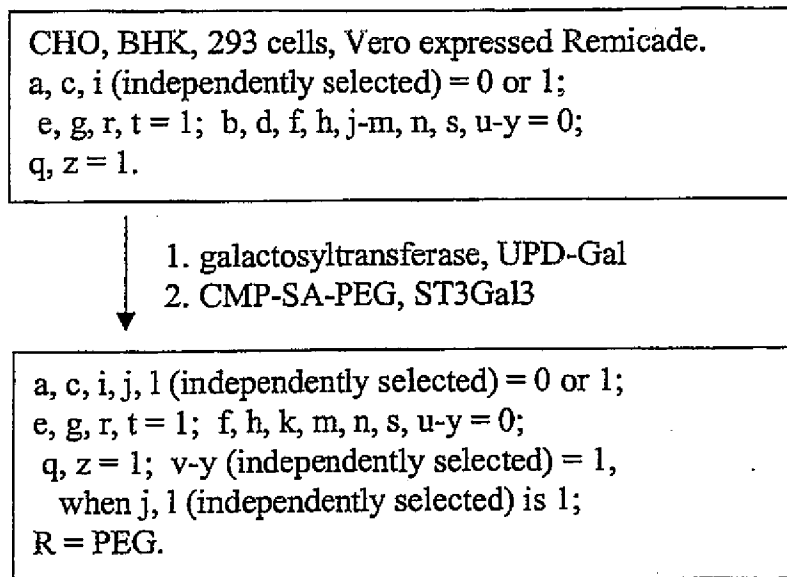


FIG. 51B

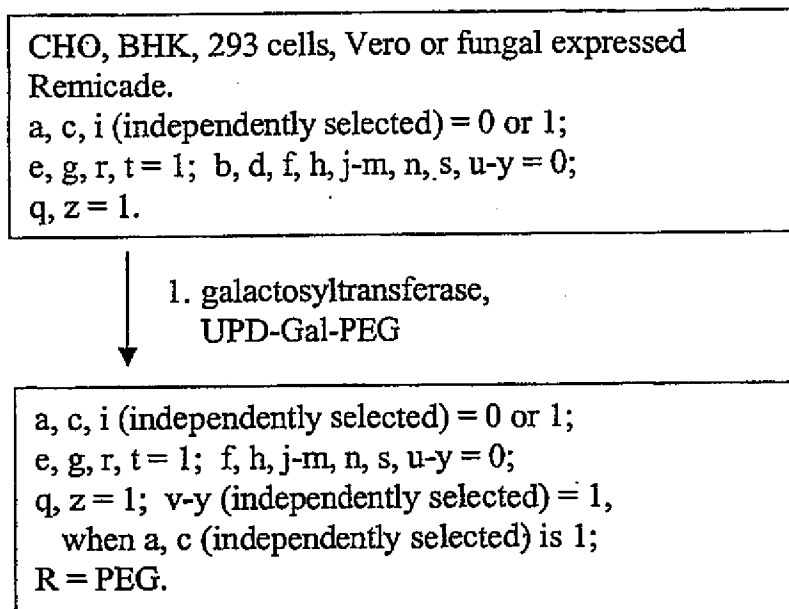


FIG. 51C



234/497

Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

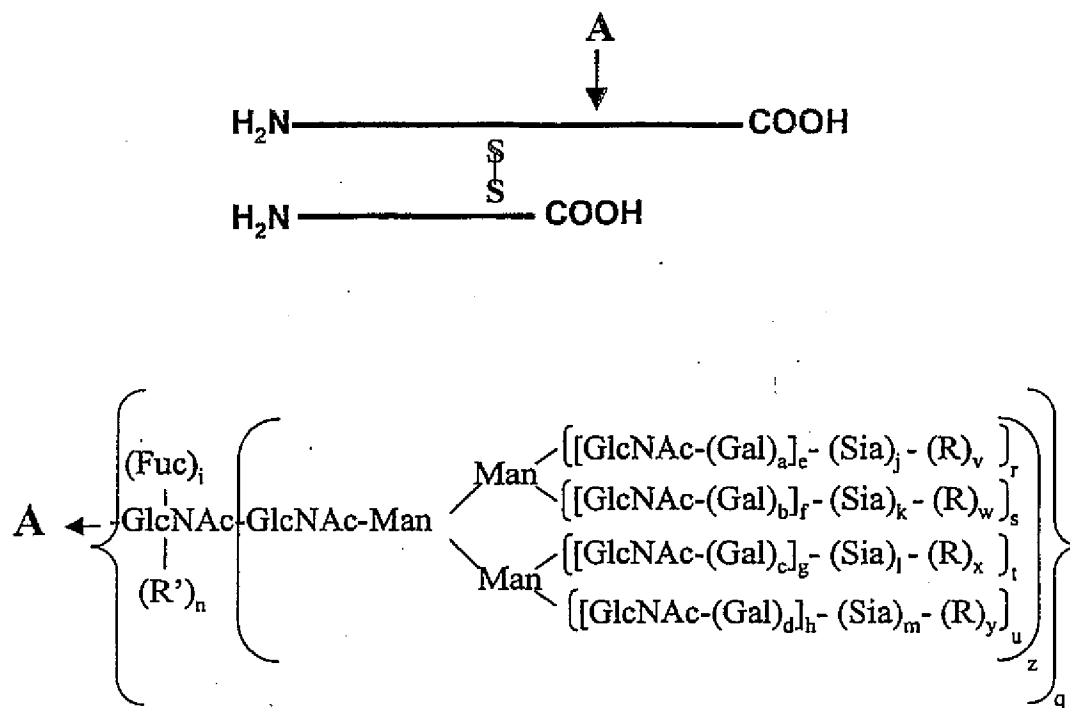
- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z= 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D

235/497



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 52A

236/497

CHO, BHK, 293 cells, Vero expressed Reopro.  
 a-m, r-u (independently selected) = 0 or 1;  
 n = 0; v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;  
 v-y (independently selected) = 1,  
 when j-m (independently selected) is 1;  
 n = 0; R = PEG; z = 1.

FIG. 52B

Insect cell expressed Reopro.  
 a-h, j-n, s-y = 0; i, r (independently selected) = 0 or 1;  
 z = 1.



1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;  
 e, g, i, r, t, v, x (independently selected) = 0 or 1;  
 v, x (independently selected) = 1,  
 when e, g (independently selected) is 1;  
 z = 1; R = PEG.

FIG. 52C

237/497

Yeast expressed Reopro.

$a-n = 0$ ;  $r-y$  (independently selected) = 0 to 1;

$z = 1$ ;

$R$  (branched or linear) = Man, oligomannose or polysaccharide.

1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

$a-m, r-z = 0$ ;  $n = 1$ ;  $R' = -\text{Gal-PEG}$ .

FIG. 52D

238/497

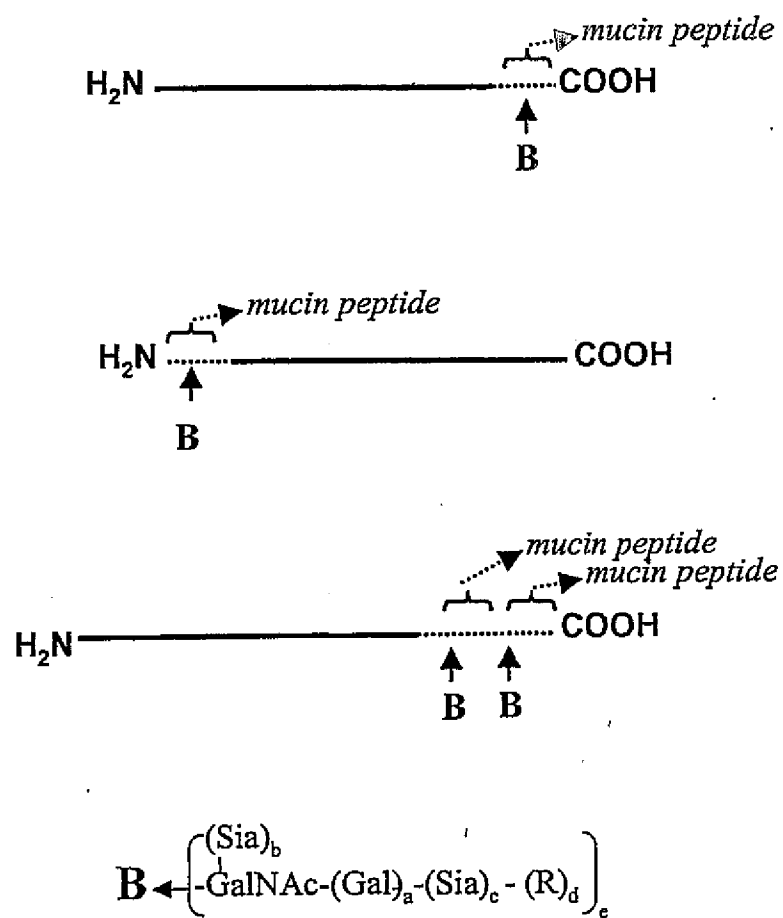


FIG. 52E

239/497

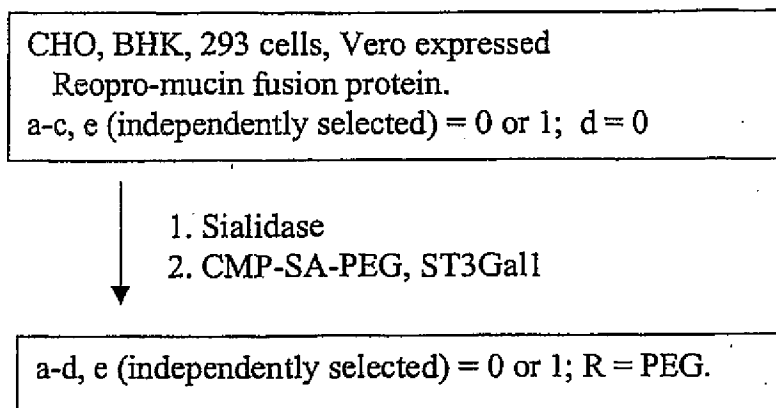


FIG. 52F

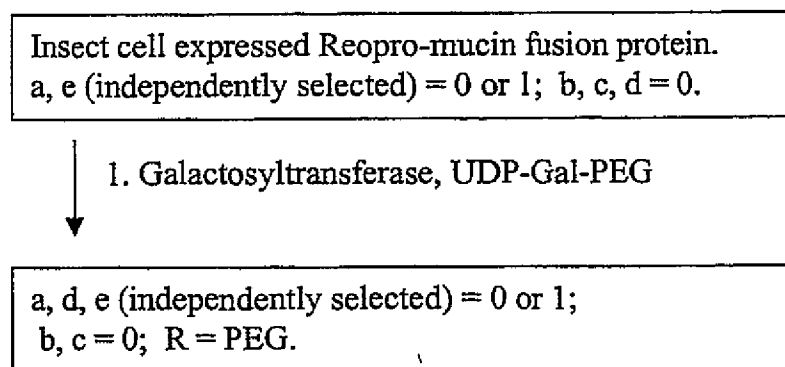


FIG. 52G

240/497

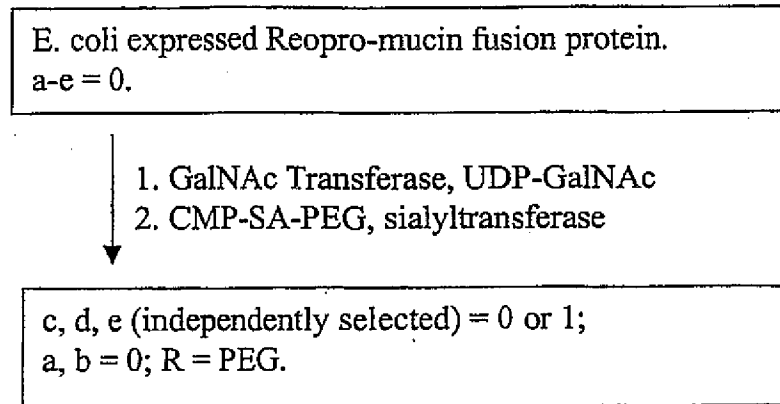
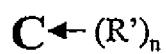
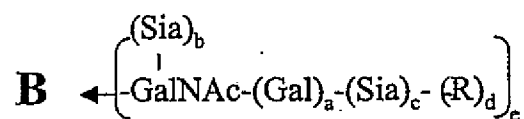
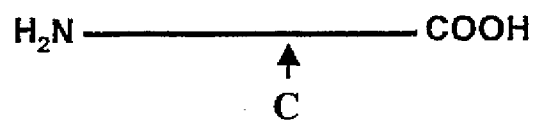
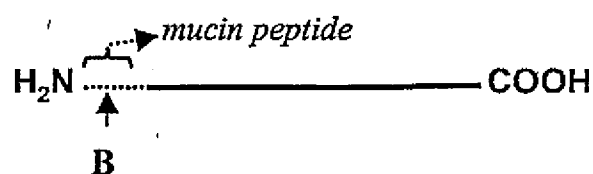


FIG. 52H

241/497



a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer, linker.

FIG. 52I



242/497

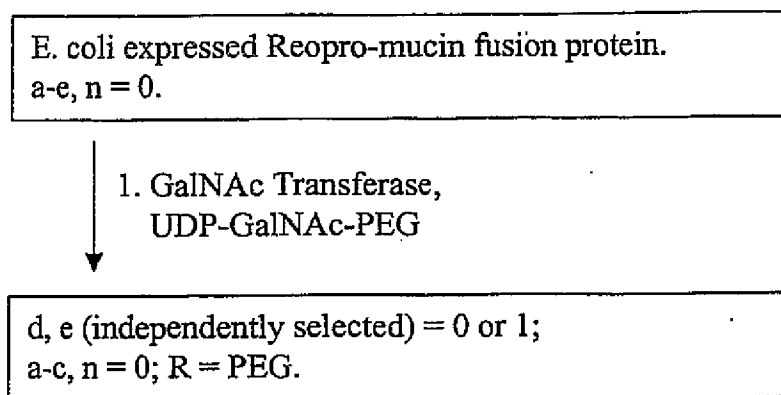


FIG. 52J

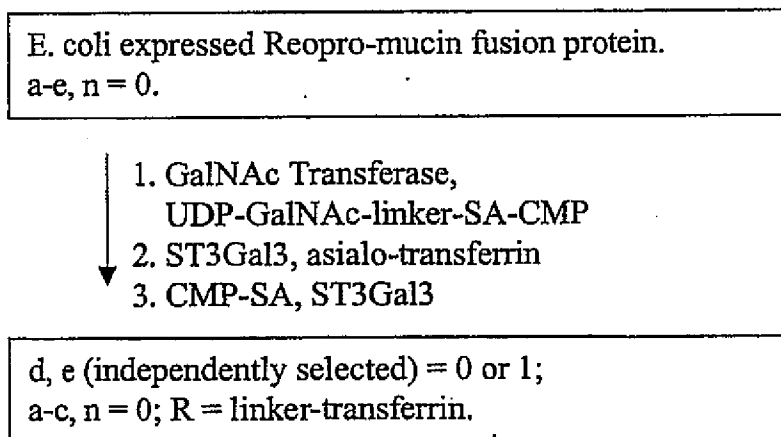


FIG. 52K

243/497

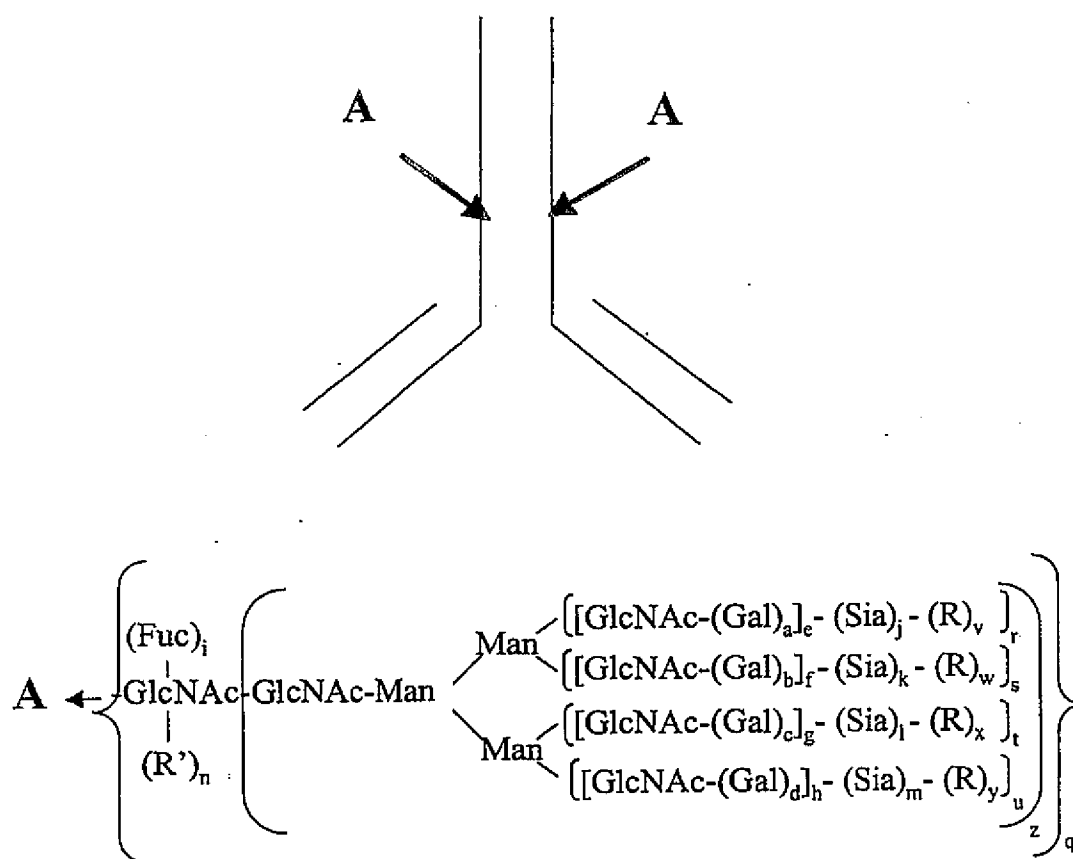
E. coli expressed Reopro(N)—no mucin peptide.  
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
  2. ST3Gal3, asialo-transferrin
  3. CMP-SA, ST3Gal3

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 52L

244/497



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

$$j-m \text{ (independently selected)} = 0 \text{ or } 1.$$

n, v-y=0; z=0 or 1; R=polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

**2**

FIG. 53A

245/497

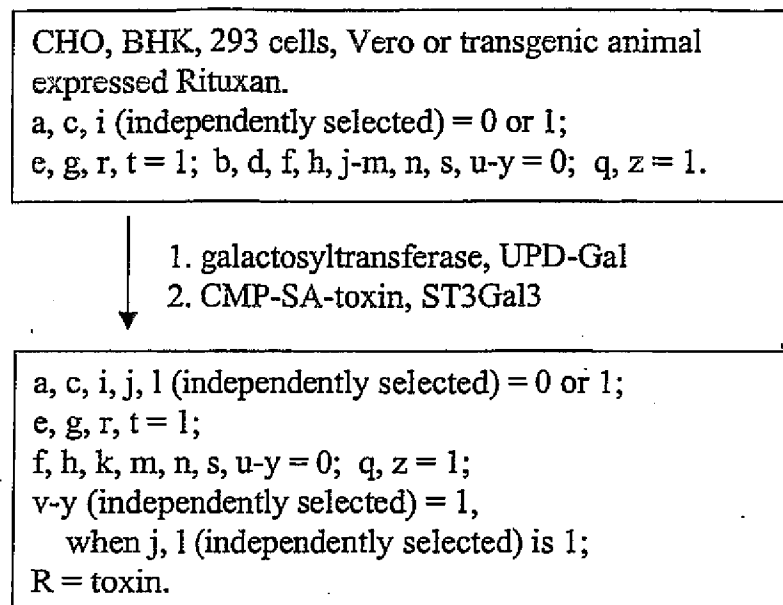


FIG. 53B

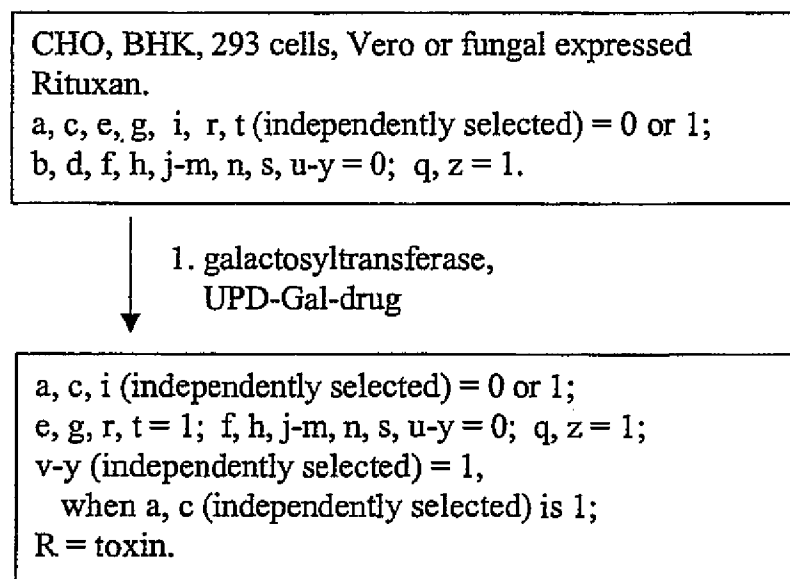


FIG. 53C

246/497

Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

2. Galactosyltransferase, UDP-Gal

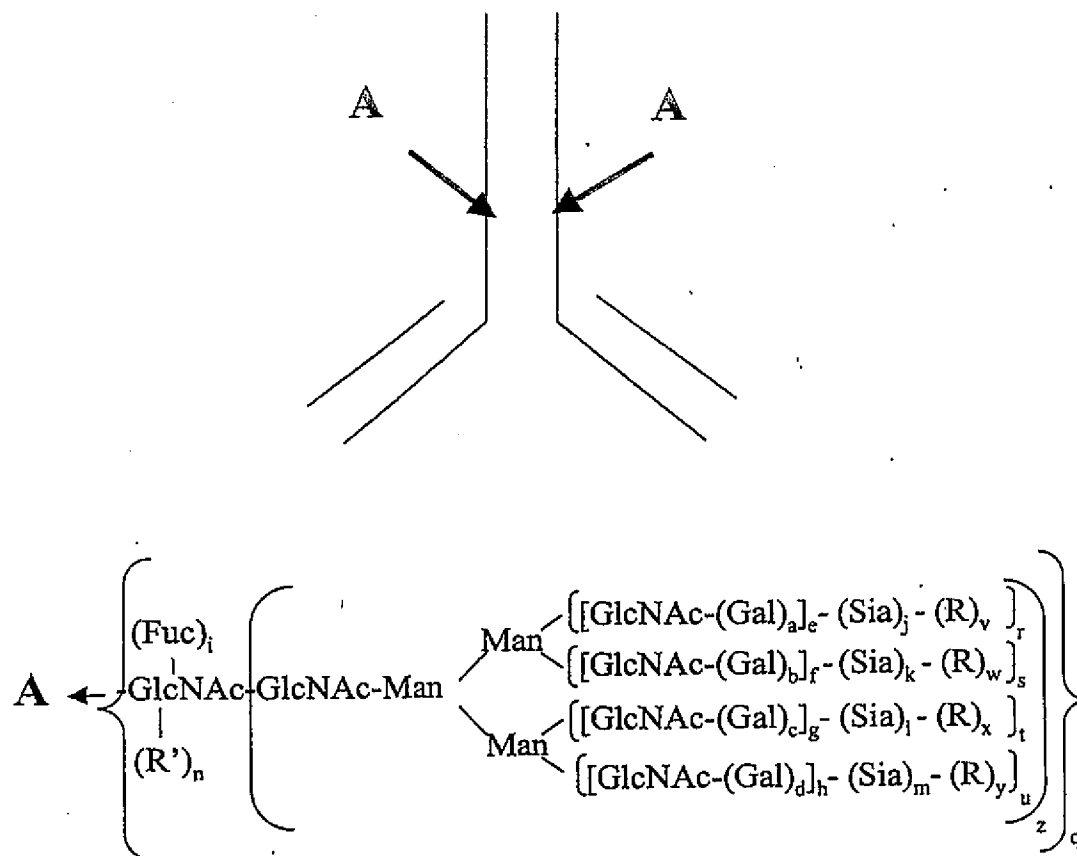
↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 53D

247/497



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug,  
glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 53E

248/497

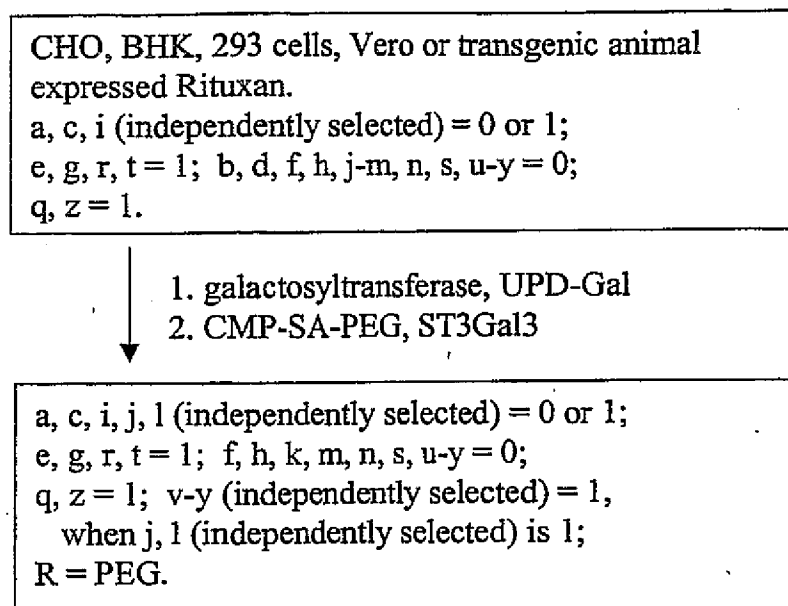


FIG. 53F

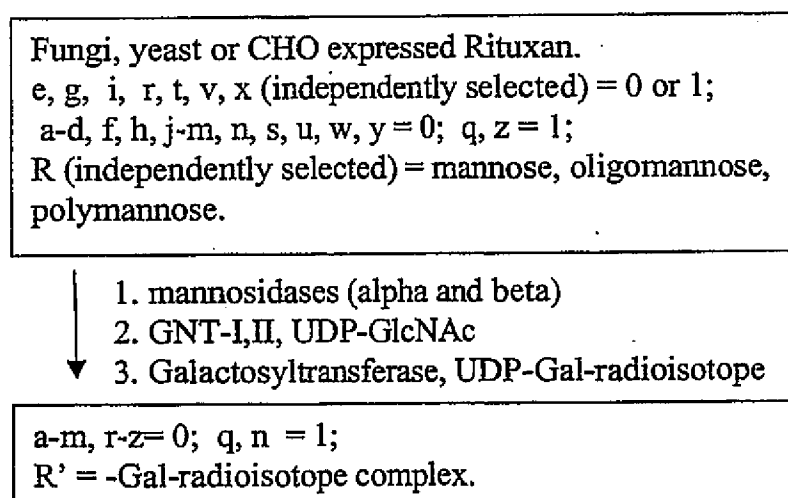
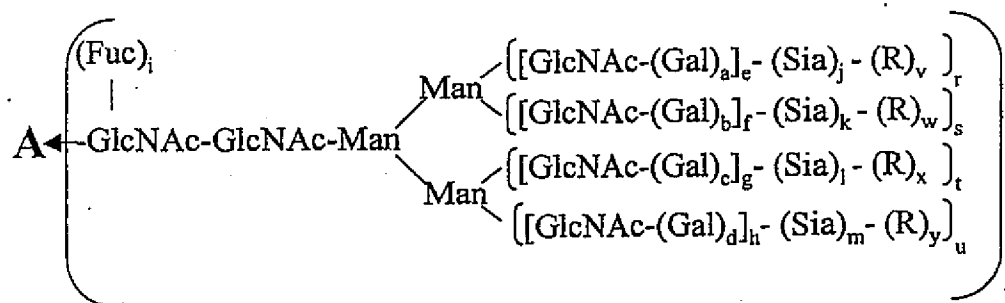
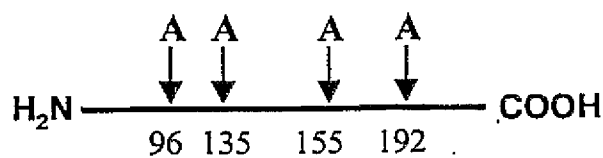


FIG. 53G

249/497



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = mannose, polymer.

FIG. 54A



250/497

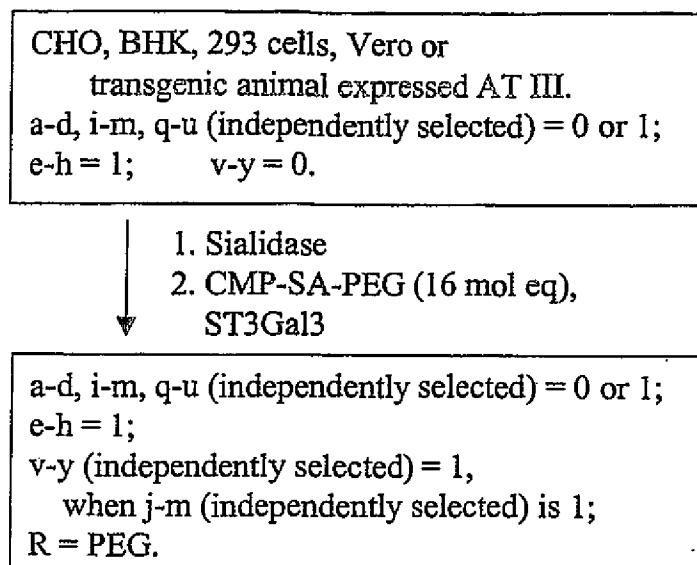


FIG. 54B

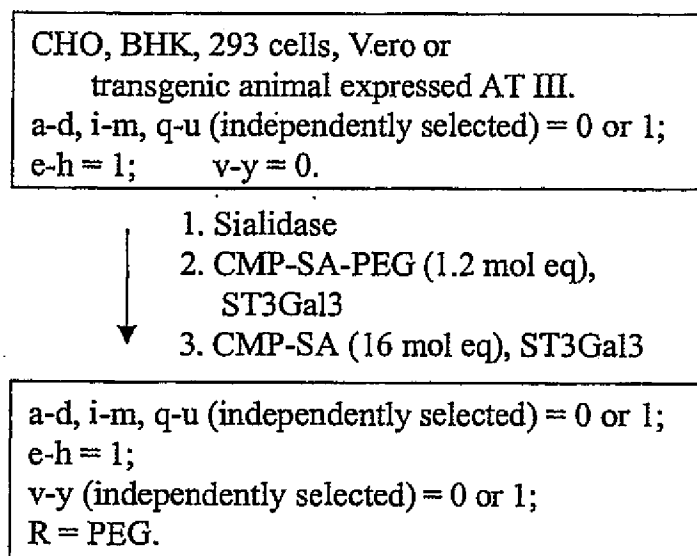


FIG. 54C

251/497

NSO expressed AT III.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1;

v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 54D

CHO, BHK, 293 cells, Vero or

transgenic animal expressed AT III.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1;

v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 54E

252/497

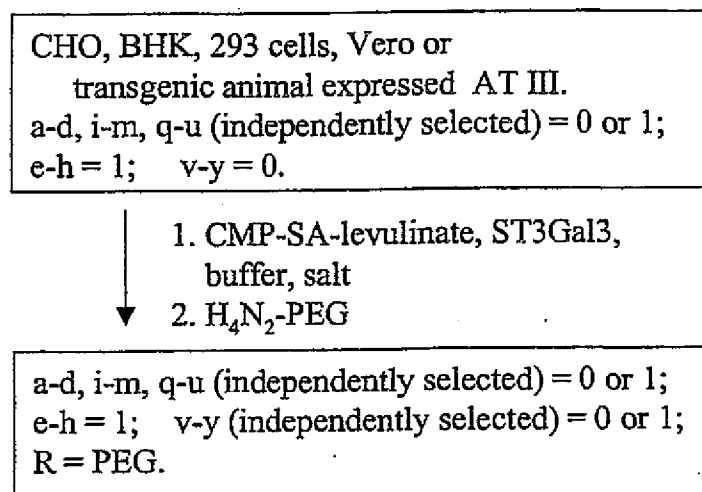


FIG. 54F

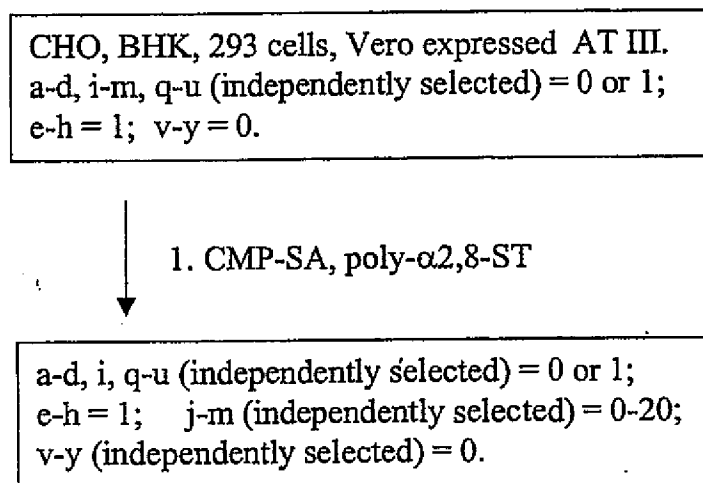
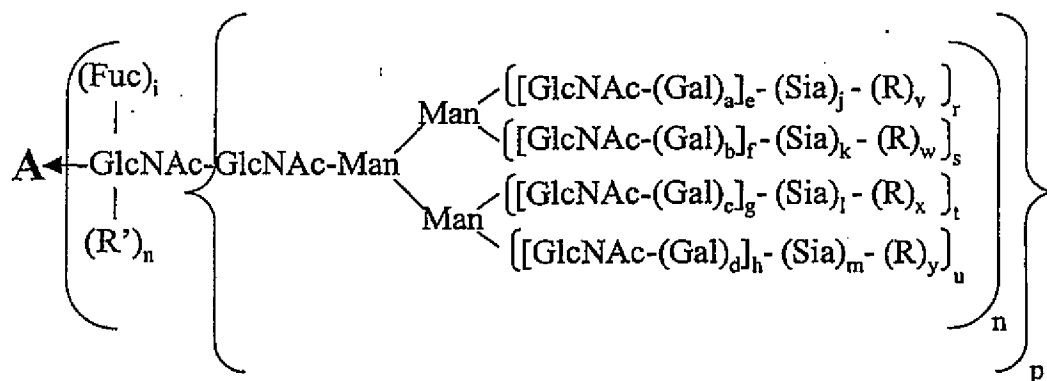
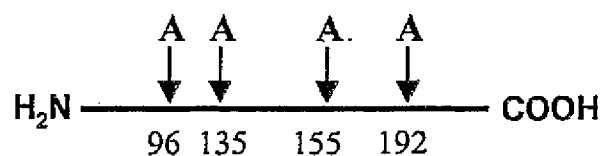


FIG. 54G

253/497



a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100.

R = polymer, linker, mannose.

$R' = H, \text{ sugar, glycoconjugate.}$

FIG. 54H

254/497

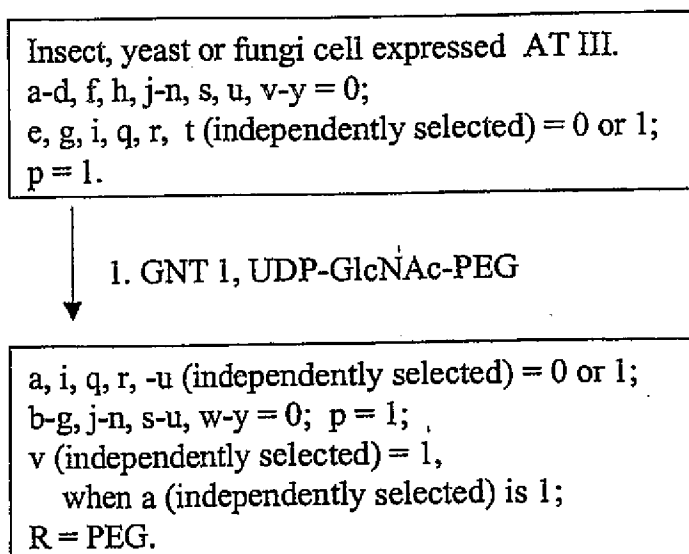


FIG. 54I

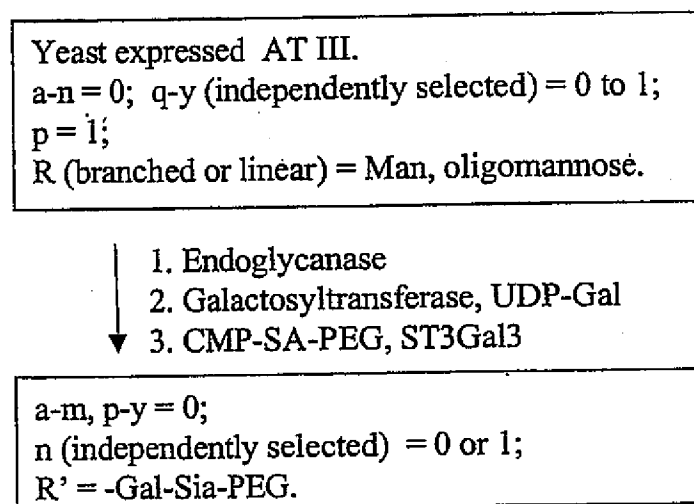


FIG. 54J

255/497

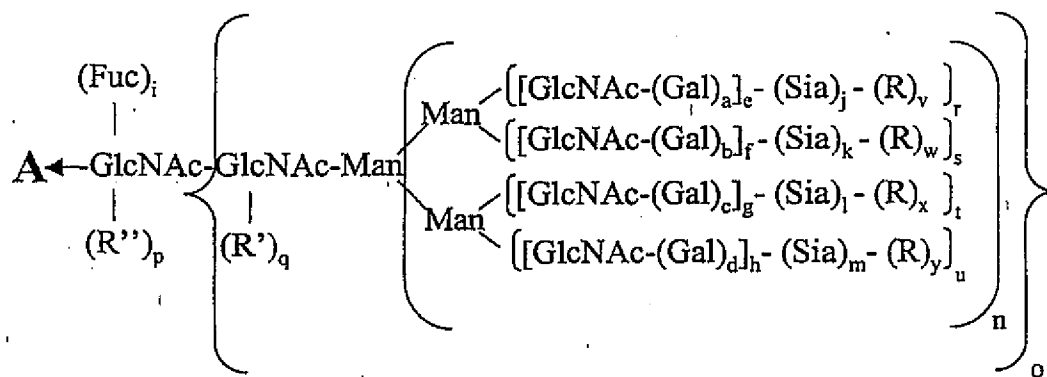
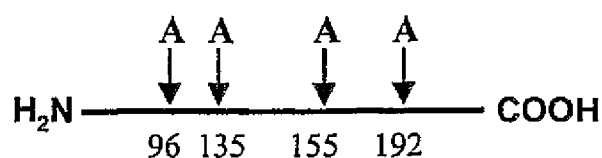
CHO, BHK, 293 cells, Vero expressed AT III.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, transferrin  
treated with endoglycanase

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 54K

256/497



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer.

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 54L

257/497

Yeast expressed AT III.

a-h, i-m, p, q = 0;

R (independently selected) = mannose,  
oligomannose, polymannose;

r-u, v-y (independently selected) = 0 or 1;

n, o = 1.

- ↓ 1. endoglycanase  
↓ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.

R'' = Gal-PEG.

FIG. 54M

Plant expressed AT III.

a-d, f-h, j-m, p, s-u, v-y = 0;

e, i, q, r (independently selected) = 0 or 1;

n, o = 1; R' = xylose.

- ↓ 1. xylosidase  
↓ 3. Galactosyl transferase, UDP-Gal-PEG

b-d, f-h, j-m, p, q, s-u, w-y = 0;

a, e, i, r (independently selected) = 0 or 1;

n, o = 1; R = PEG.

FIG. 54N



258/497

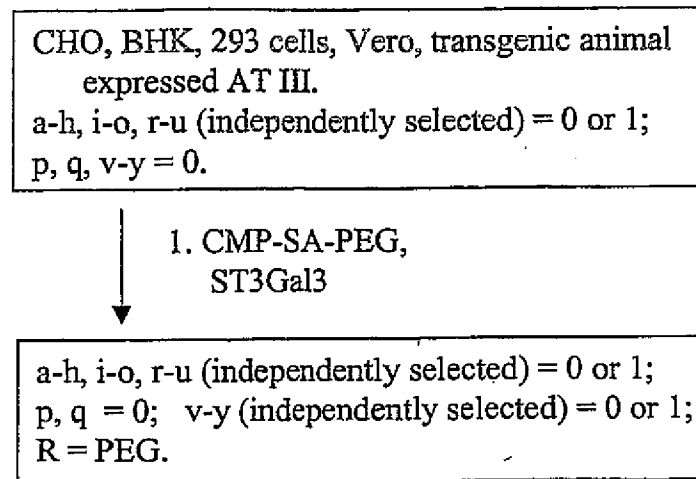
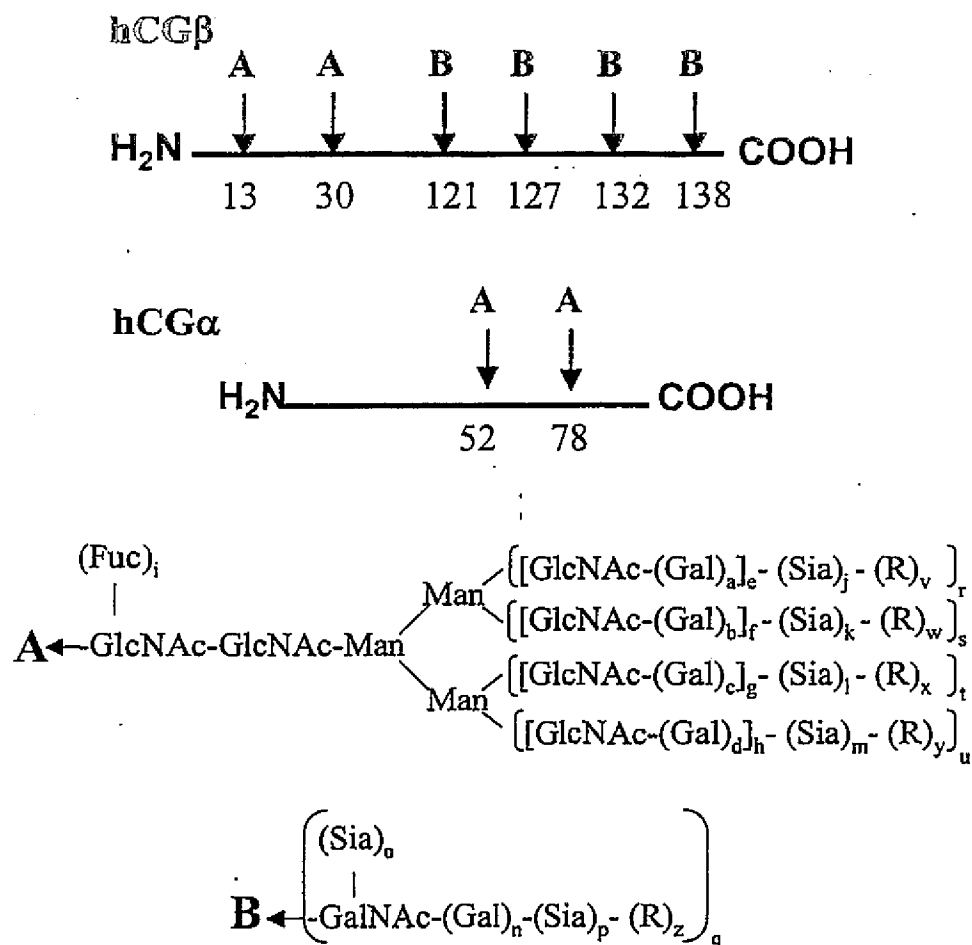


FIG. 54O

259/497



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; R = polymer

FIG. 55A

260/497

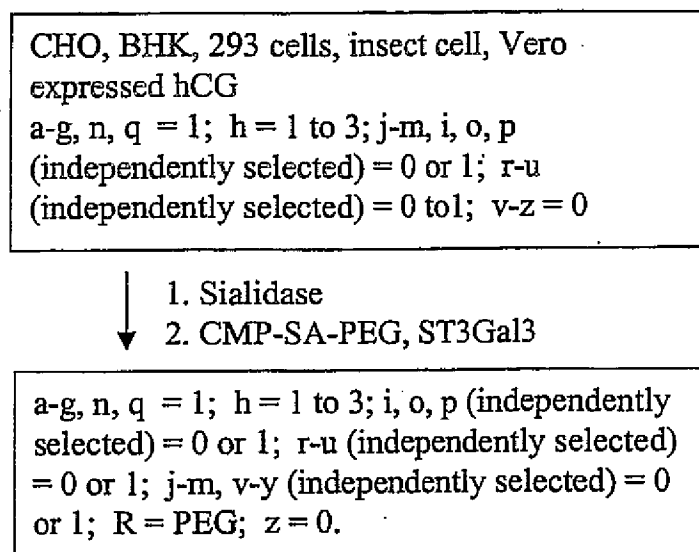


FIG. 55B

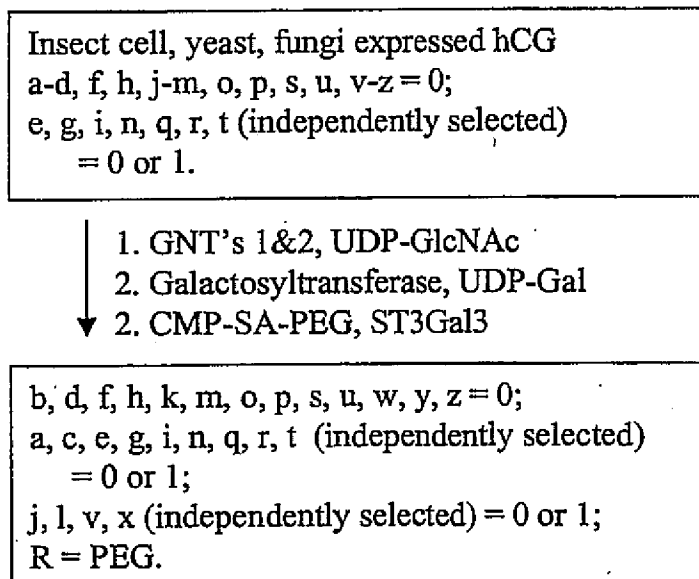


FIG. 55C

261/497

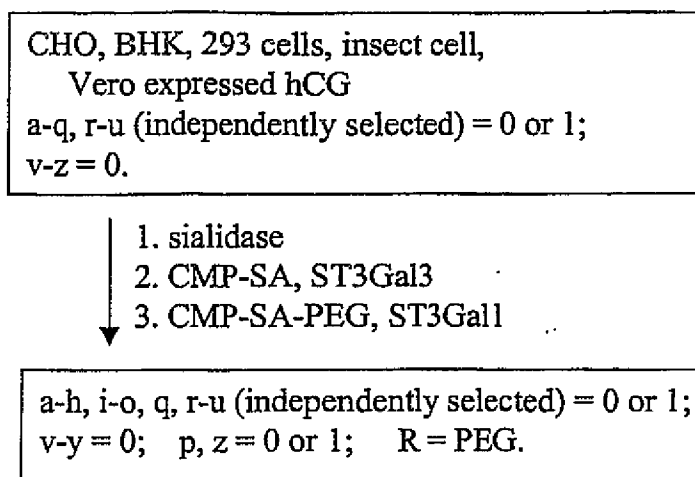


FIG. 55D

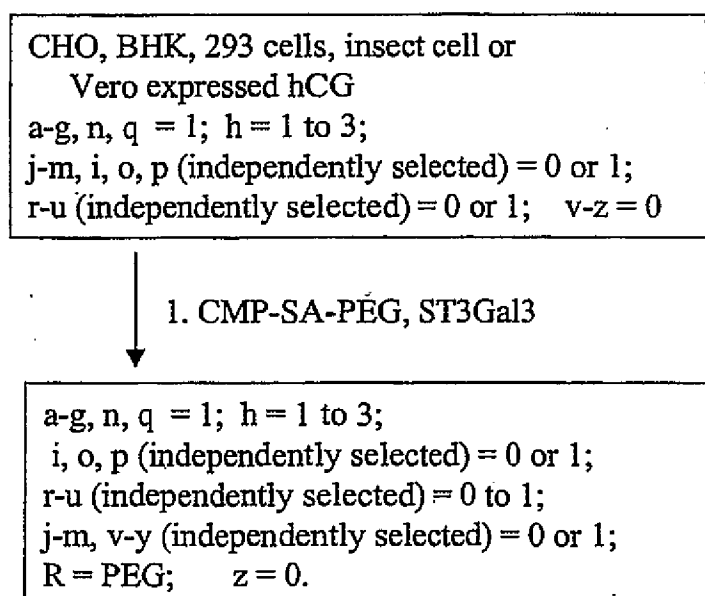


FIG. 55E

262/497

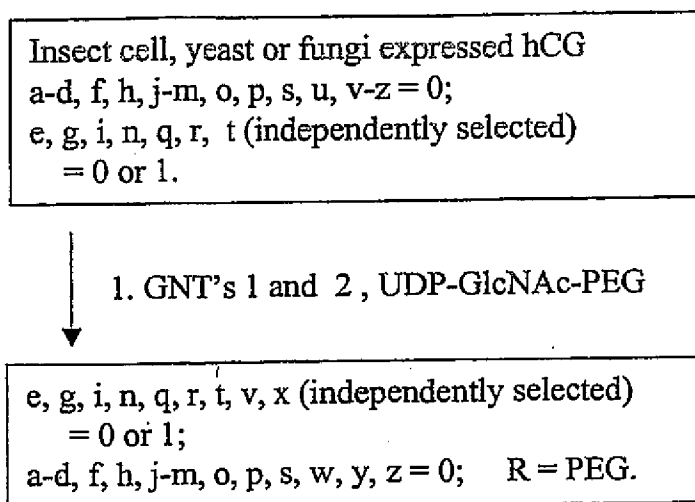


FIG. 55F

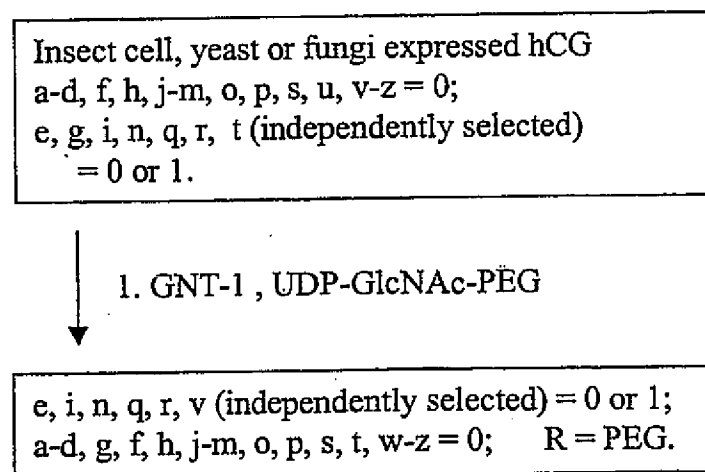


FIG. 55G

263/497

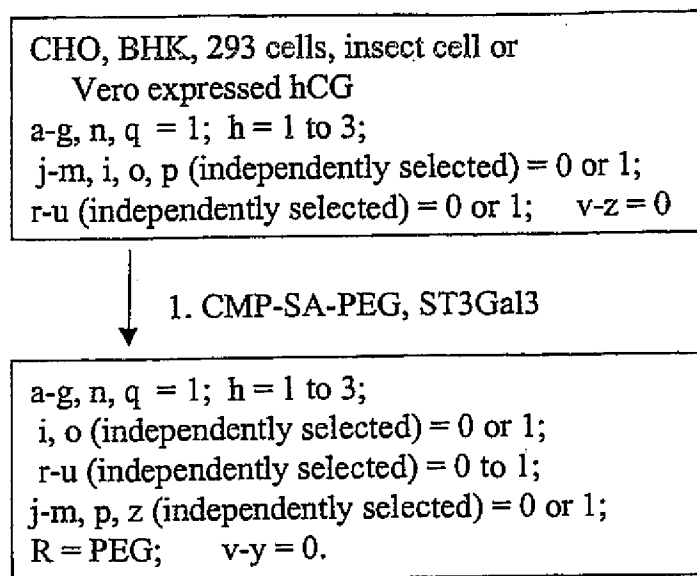


FIG. 55H

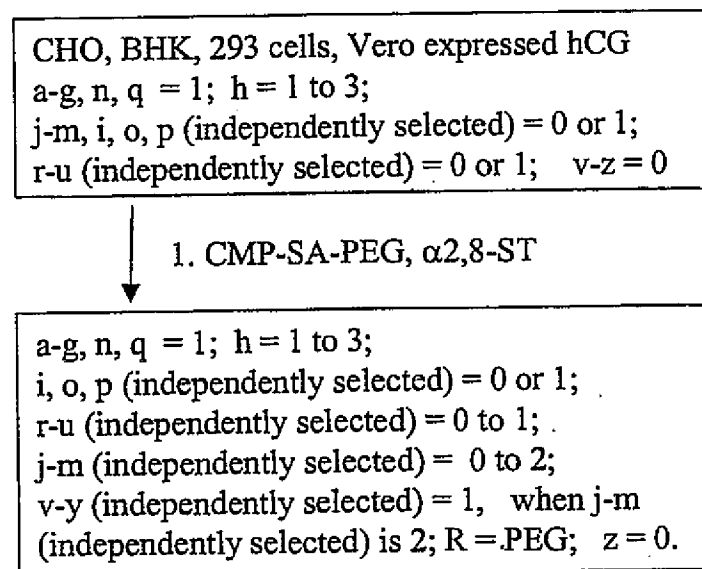


FIG. 55I

264/497

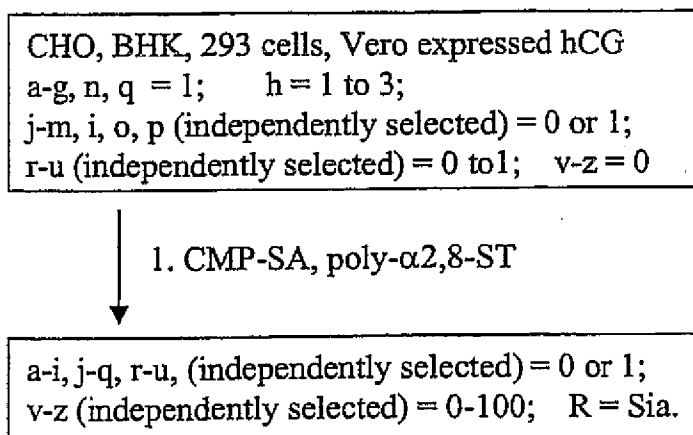
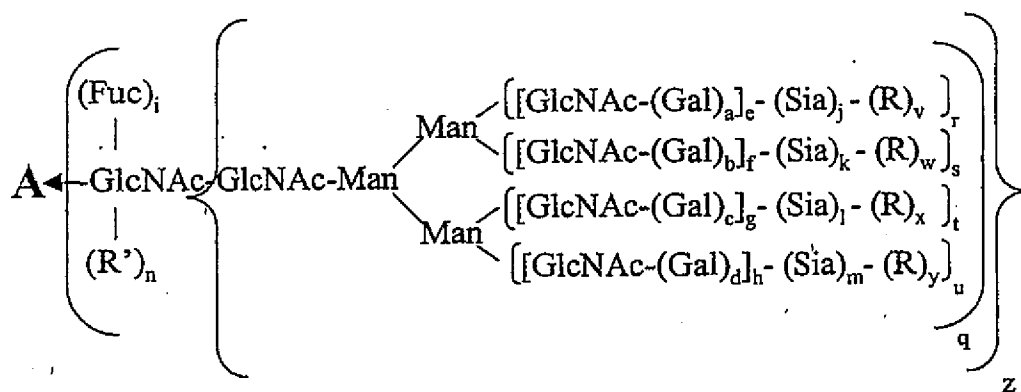
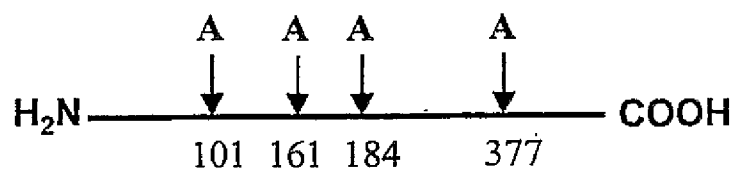


FIG. 55J

265/497



a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 56A



266/497

CHO, BHK, 293 cells, insect cells, Vero expressed  
and secreted alpha-galactosidase  
a-h, i-m, q-u (independently selected) = 0 or 1;  
z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Endo-H  
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;  
n, v-y = 0; z = 1; and when z = 0 and q = 1,  
then n (independently selected) = 0 or 1;  
R' = Gal-PEG-transferrin.

FIG. 56B

CHO, BHK, 293 cells, Insect cells,  
Vero expressed and secreted alpha-galactosidase  
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1; n, v-y  
= 0; and when a-n = 0, then r-u (independently selected) = 0  
or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Sialidase  
2. CMP-SA-linker-Mannose-6-phosphate  
ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1;  
n = 0; z = 1; R = mannose-6-phosphate; and when a-n  
= 0, then r-u (independently selected) = 0 or 1;  
v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

FIG. 56C

267/497

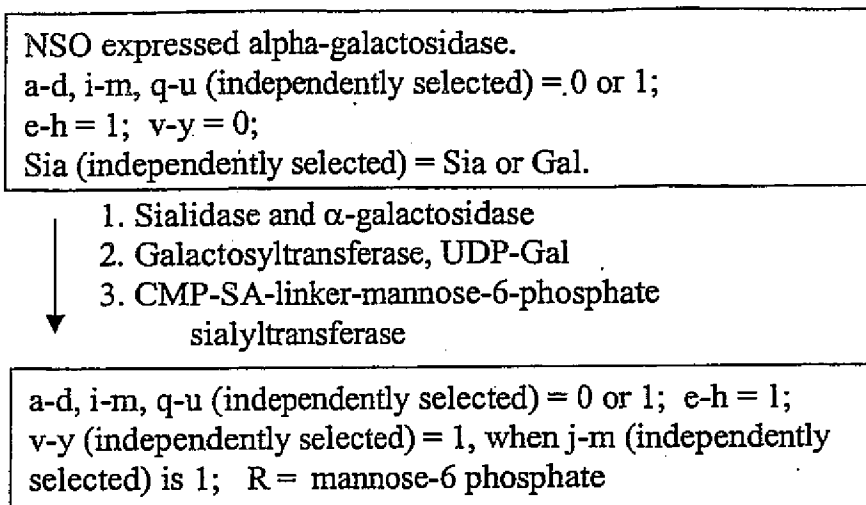


FIG. 56D

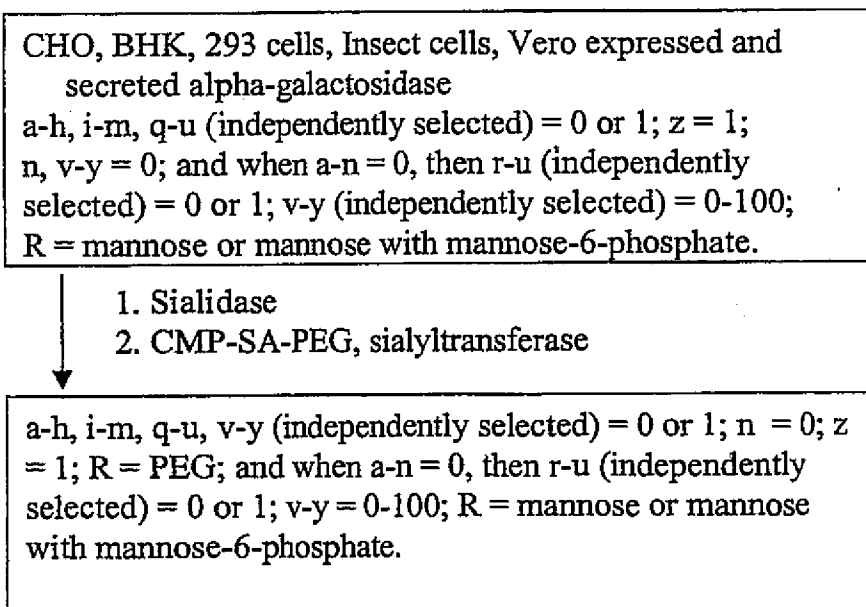


FIG. 56E

268/497

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-galactosidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,  
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate;  
v-y (independently selected) = 0 or 1;  
R = mannose-linker-ApoE.

FIG. 56F

CHO, BHK, 293 cells, Insect cells, Vero, yeast,  
fungi expressed alpha-galactosidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H  
2. galactosyltransferase,  
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;  
R' = galactose-linker-alpha2-macroglobulin.

FIG. 56G

269/497

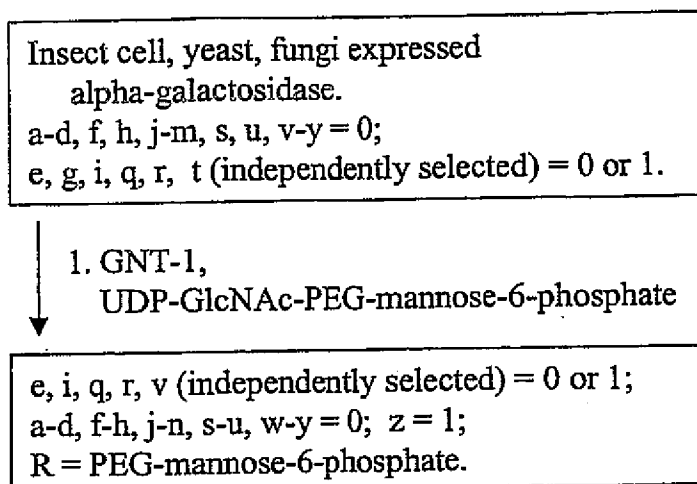


FIG. 56H

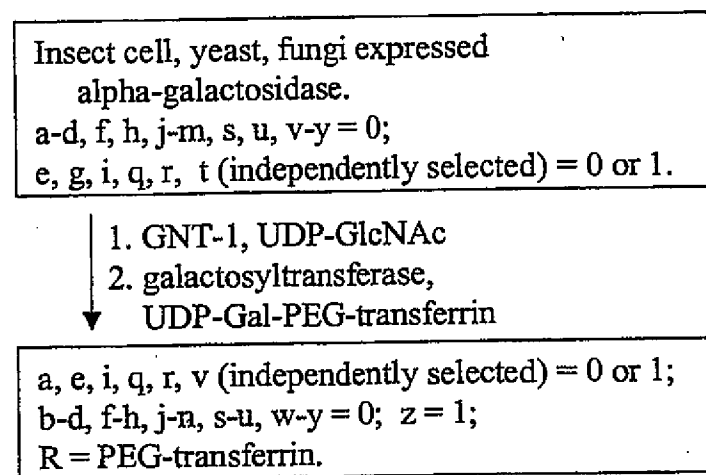


FIG. 56I

270/497

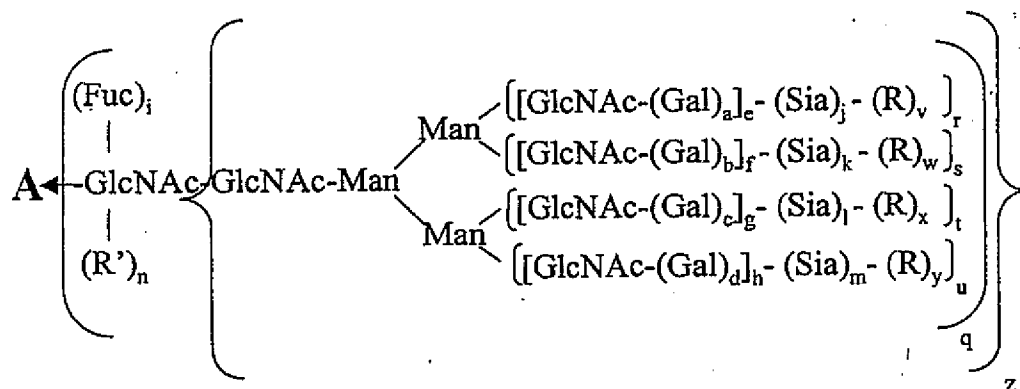
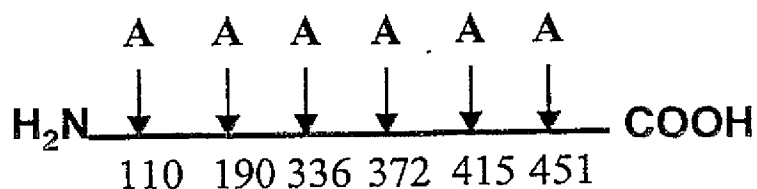
Insect cell, yeast, fungi expressed  
alpha-galactosidase.  
a-d, f, h, j-m, s, u, v-y = 0;  
e, g, i, q, r, t (independently selected) = 0 or 1.

- ↓  
1. GNT-1 and 2, UDP-GlcNAc  
2. galactosyltransferase, UDP-Gal  
3. sialyltransferase,  
CMP-SA-PEG-melanotransferrin

a, c, e, g, i, j, l, q, r, t, v, x (independently  
selected) = 0 or 1;  
b, d, f, h, k, m, n, s, u, w, y = 0;  
z = 1; R = PEG-melanotransferrin.

FIG. 56J

271/497



a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 57A

272/497

CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase  
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Endo-H  
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;  
n, v-y = 0; z = 1; and when z = 0 and q = 1, then n  
(independently selected) = 0 or 1; R' = Gal-PEG-transferrin.

FIG. 57B

CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase  
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Sialidase  
2. CMP-SA-linker-Mannose-6-phosphate ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;  
z = 1; R = mannose-6-phosphate; and when a-n = 0,  
then r-u (independently selected) = 0 or 1;  
v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

FIG. 57C

273/497

NSO expressed alpha-iduronidase.

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;  
v-y = 0; Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = mannose-6 phosphate

FIG. 57D

CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
  2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;  
z = 1; R = PEG; and when a-n = 0, then r-u  
(independently selected) = 0 or 1; v-y = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

FIG. 57E



274/497

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-iduronidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,  
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1; j-m (independently  
selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate;  
v-y (independently selected) = 0 or 1;  
R = mannose-linker-ApoE.

FIG. 57F

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-iduronidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1;  
z = 1; r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H  
2. galactosyltransferase,  
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;  
R' = galactose-linker-alpha2-macroglobulin.

FIG. 57G

275/497

Insect cell, yeast, fungi expressed  
alpha-iduronidase.  
a-d, f, h, j-m, s, u, v-y = 0;  
e, g, i, q, r, t (independently selected) = 0 or 1.

↓  
1. GNT-1,  
UDP-GlcNAc-PEG-mannose-6-phosphate

e, i, q, r, v (independently selected) = 0 or 1;  
a-d, f-h, j-n, s-u, w-y = 0; z = 1;  
R = PEG-mannose-6-phosphate.

FIG. 57H

Insect cell, yeast, fungi expressed  
alpha-iduronidase.  
a-d, f, h, j-m, s, u, v-y = 0;  
e, g, i, q, r, t (independently selected) = 0 or 1.

↓  
1. GNT-1, UDP-GlcNAc  
2. galactosyltransferase,  
UDP-Gal-PEG-transferrin

a, e, i, q, r, v (independently selected) = 0 or 1;  
b-d, f-h, j-n, s-u, w-y = 0; z = 1;  
R = PEG-transferrin.

FIG. 57I

276/497

Insect cell, yeast, fungi expressed  
alpha-iduronidase.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.

- ↓  
1. GNT-1 and 2, UDP-GlcNAc  
2. galactosyltransferase, UDP-Gal  
3. sialyltransferase,  
CMP-SA-PEG-melanotransferrin

a, c, e, g, i, j, l, q, r, t, v, x

(independently selected) = 0 or 1;

b, d, f, h, k, m, n, s, u, w, y = 0; z = 1;

R = PEG-melanotransferrin.

FIG. 57J

277/497

FIG. 58A

ACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT  
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG  
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGT  
GCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTG  
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA  
GCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGATCT  
CCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCG  
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC  
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCT  
TTCCAGCGCCGGGCAGGAGGGGTCCTGGTTGCCTCCCATCTGCAGAG  
CTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTG  
A

FIG. 58B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu  
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr  
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro  
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser  
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile  
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe  
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro  
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val  
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His  
Leu Ala Gln Pro

278/497

FIG. 59A

GCGCCTCTTATGTACCCACAAAAATCTATTTTCAAAAAAGTTGCTCTA  
AGAATATAGTTATCAAGTTAAGTAAAATGTCAATAGCCTTTTAATTTA  
ATTTTAAATTGTTTTATCATTCTTTGCAATAATAAACATTAACCTTTAT  
ACTTTTAAATTTAATGTATAGAATAGAGATATACATAGGATATGTAAA  
TAGATACACAGTGTATATGTGATTAAAATATAATGGGAGATTCAATC  
AGAAAAAAGTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAGGAAAC  
AATAATGAAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTA  
AAGAGTGTATAAAGAAAGCAAAAAGAGAAGTAGAAAGTAACACAGG  
GGCATTGGAATAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC  
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC  
CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA  
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT  
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCCTGGGTTAGCAGG  
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAATCTCTCTTTTCTCC  
TGCTTGAAGGACAGACATGACTTTGGATTTCCCCAGGAGGAGTTTGG  
CAACCAGTTCCAAAAGGCTGAAACCATCCCTGTCCTCCATGAGATGA  
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT  
GGGATGAGACCCTCCTAGACAAATTCTACACTGAACTCTACCAGCAG  
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGA  
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT  
TCCAAAGAATCACTCTCTATCTGAAAGAGAAGAAATACAGCCCTTGT  
GCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCTTTTTCTTTGTCA  
ACAACTTGCAAGAAAGTTTAAGAAGTAAGGAATGAAAAGTGGTTCA  
ACATGGAAATGATTTTTCATTGATTCGTATGCCAGCTCACCTTTTTATG  
ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT  
TAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACATTGTATTGAG  
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATGCTGACTGATCCATT  
ATCTATTTAAATATTTTTAAAATATTATTTATTTAACTATTTATAAAAC  
AACTTATTTTTGTTTCATATTATGTCATGTGCACCTTTGCACAGTGGTTA  
ATGTAATAAAATGTGTTCTTTGTATTTGGTAAATTTATTTTGTGTGTT  
CATTGAACTTTTGCTATGGAACCTTTGTACTTGTTTATTCTTTAAAATG  
AAATTCCAAGCCTAATTGTGCAACCTGATTACAGAATAACTGGTACA  
CTTCATTTGTCCATCAATATTATTTCAAGATATAAGTAAAAATAAAC  
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACC  
TAACAAATACAATTCTGCTCTCTTGTGTATTTGATTTTTGTATGAAAA  
AACTAAAAATGGTAATCATACTTAATTATCAGTTATGGTAAATGGT  
ATGAAGAGAAGAAGGAACG

FIG. 59B

279/497

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser  
Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr  
Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala  
Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr  
Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu  
Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val  
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe  
Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val  
Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu  
Arg Ser Lys Glu

FIG. 59C

ATGGCCCTCCTGTTCCCTCTACTGGCAGCCCTAGTGATGACCAGCTAT  
AGCCCTGTTGGATCTCTGGGCTGTGATCTGCCTCAGAACCATGGCCTA  
CTTAGCAGGAACACCTTGGTGCTTCTGCACCAAATGAGGAGAATCTCC  
CCTTTCTTGTGTCTCAAGGACAGAAGAGACTTCAGGTTCCCCCAGGAG  
ATGGTAAAAGGGAGCCAGTTGCAGAAGGCCCATGTCATGTCTGTCTCT  
CCATGAGATGCTGCAGCAGATCTTCAGCCTCTTCCACACAGAGCGCTC  
CTCTGCTGCCTGGAACATGACCCTCCTAGACCAACTCCACACTGGACT  
TCATCAGCAACTGCAACACCTGGAGACCTGCTTGCTGCAGGTAGTGG  
GAGAAGGAGAATCTGCTGGGGCAATTAGCAGCCCTGCACTGACCTTG  
AGGAGGTA CTTCAGGGAATCCGTGTCTACCTGAAAGAGAAGAAATA  
CAGCGACTGTGCCTGGGAAGTTGTCAGAATGGAAATCATGAAATCCT  
TGTTCTTATCAACAAACATGCAAGAAAGACTGAGAAGTAAAGATAGA  
GACCTGGGCTCATCTTGA

FIG. 59D

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr Ser Pro Val  
Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg Asn Thr  
Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu Cys Leu Lys Asp  
Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys Gly Ser Gln Leu Gln Lys  
Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His  
Thr Glu Arg Ser Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr  
Gly Leu

280/497

FIG. 60A

ATGACCAACAAGTGTCTCCTCCAAATTGCTCTCCTGTTGTGCTTCTCC  
ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCTACAAAGA  
AGCAGCAATTTTCAGTGTGAGAAGCTCCTGTGGCAATTGAATGGGAG  
GCTTGAATATTGCCTCAAGGACAGGATGAACTTTGACATCCCTGAGG  
AGATTAAGCAGCTGCAGCAGTTCCAGAAGGAGGACGCCGCATTGACC  
ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA  
TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA  
TGTCTATCATCAGATAAACCATCTGAAGACAGTCCTGGAAGAAAAAC  
TGGAGAAAGAAGATTTTACCAGGGGAAACTCATGAGCAGTCTGCAC  
CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA  
GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAAATCCTAAGGA  
ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT  
CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTTCAAGCATTCTTC  
AACCAGCAGATGCTGTTTAAGTGACTGATGGCTAATGTACTGCAAAT  
GAAAGGACACTAGAAGATTTTGAAATTTTATTAAATTATGAGTTATT  
TTTATTTAT TTAAATTTTATTTTGGAAAATAAATTATTTTGGTGC

FIG. 60B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala  
Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp  
Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu  
Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln  
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val  
Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp  
Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile  
Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val  
Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

281/497

FIG. 61A

ATGGTCTCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG  
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCACGGCGT  
CCTGCACCGGCGCCGGCGCGCCAACGCGTTCCTGGAGGAGCTGCGGC  
CGGGCTCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA  
GGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC  
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA  
GAATGGGGGCTCCTGCAAGGACCAGTCCAGTCCATATCTGCTTCT  
GCCTCCCTGCCTTCGAGGGGCCGGAACGTGTGAGACGCACAAGGATGAC  
CAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAGCAGTACTGCAG  
TGACCACACGGGCACCAAGCGCTCCTGTCTGGTGCCACGAGGGGTACT  
CTCTGCTGGCAGACGGGGTGTCTTGCACACCCACAGTTGAATATCCA  
TGTGGAAAAATACCTATTCTAGAAAAAAGAAATGCCAGCAAACCCCA  
AGGCCGAATTGTGGGGGGCAAGGTGTGCCCCAAAGGGGAGTGTCCA  
TGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC  
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA  
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC  
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG  
TCATCATCCCCAGCACGTACGTCCCGGGCACCACCAACCACGACATC  
GCGCTGCTCCGCCTGCACCAGCCCGTGGTCTCACTGACCATGTGGTG  
CCCCTCTGCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC  
GTGCGCTTCTCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGG  
CGCCACGGCCCTGGAGCTCATGGTGTCAACGTGCCCCGGCTGATGA  
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT  
ATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA  
CTCCTGCAAGGGGGACAGTGGAGGCCCCACATGCCACCCACTACCGGG  
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCA  
ACCGTGGGGCCACTTTGGGGTGTACACCAGGGTCTCCAGTACATCGA  
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCCAGGAGTCCTCC  
TGCGAGCCCCATTCCC



282/497

FIG. 61B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys  
Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val Leu His Arg Arg Arg  
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys  
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg  
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys  
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro  
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val  
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg  
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro  
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys  
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln  
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile  
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile  
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg  
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp  
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu  
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser  
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu  
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg  
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp  
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg  
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly  
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met  
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

283/497

FIG. 62A

ATGCAGCGCGTGAACATGATCATGGCAGAATCACCAAGCCTCATCAC  
CATCTGCCCTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTTTCTT  
GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA  
TTCAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAAT  
GTATGGAAGAAAAGTGTAGTTTTTGAAGAACCACGAGAAGTTTTTGAA  
AACACTGAAAAGACAACCTGAATTTTGAAGCAGTATGTTGATGGAGA  
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG  
ACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGA  
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG  
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT  
GAGGGATATCGACTTGCAGAAAACCAGAAGTCCTGTGAACCAGCAGT  
GCCATTTCCATGTGGAAGAGTTTCTGTTTCACAACTTCTAAGCTCAC  
CCGTGCTGAGGCTGTTTTTCCTGATGTGGACTATGTAAATCCTACTGA  
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA  
ATGACTTCACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA  
TTCCCTTGGCAGGTTGTTTTGAATGGTAAAGTTGATGCATTCTGTGGA  
GGCTCTATCGTTAATGAAAAATGGATTGTAAGTGTGCTGCCCAGTGTGT  
GAAACTGGTGTAAAATTACAGTTGTTCGAGGTGAACATAATATTGA  
GGAGACAGAACATACAGAGCAAAAGCGAAATGTGATTTCGAGCAATT  
ATTCCTCACCACAACCTACAATGCAGCTATTAATAAGTACAACCATGA  
CATTGCCCTTCTGGAAGTGGACGAACCCTTAGTGCTAAACAGCTACG  
TTACACCTATTTGCATTGCTGACAAGGAATACACGAACATCTTCCTCA  
AATTTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCACAAA  
GGGAGATCAGCTTTAGTTCTTCAGTACCTTAGAGTTCCACTTGTTGAC  
CGAGCCACATGTCTTCGATCTACAAAGTTCACCATCTATAACAACAT  
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTCATGTCAAGGAG  
ATAGTGGGGGACCCCATGTTACTGAAGTGGGAAGGGACAGTTTCTTA  
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAATA  
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAGGAAA  
AAACAAAGCTCACTTAATGAAAGATGGATTTCCAAGGTTAATTCATT  
GGAATTGAAAATTAACAG

284/497

FIG. 62B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu  
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala  
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe  
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu  
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr  
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys  
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn  
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys  
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu  
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser  
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr  
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser  
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe  
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val  
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr  
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn  
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn  
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr  
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly  
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln  
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe  
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser  
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu  
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr  
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr

285/497

FIG. 63A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG  
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCCA  
GAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCC  
AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCC  
ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAG  
AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG  
GGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTG  
TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT  
GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT  
GTGAGATAAACTCTCCTTTTCCTTACCATAACCACTTTGACACGCTTC  
AAGGATATACTGCAGCTTTACTGCCTTCCTCCTTATCCTACAGTACAA  
TCAGCAGTCTAGTTCTTTTCATTTGGAATGAATACAGCATTAAAGCTTG  
TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 63B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu  
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu  
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe  
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn  
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met  
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His  
Lys Ser

286/497

FIG. 63C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC  
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA  
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTTGGTGTGCTG  
GCTACTGCTACACCAGGGATCTGGTGTATAAGGACCCAGCCAGGCCC  
AAAATCCAGAAAACATGTACCTTCAAGGAAGTGGTATATGAAACAGT  
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC  
AGTGGCCACCCAGTGTCACCTGTGGCAAGTGTGACAGCGACAGCACTG  
ATTGTACTGTGCGAGGCCTGGGGCCCAGCTACTGCTCCTTTGGTGAAA  
TGAAAGAATAA

FIG. 63D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys  
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe  
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val  
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val  
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr  
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys  
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

287/497

FIG. 64A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC  
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT  
GCACCGCCGAGCTTCCCGGGATGAGGGCCCCCGGTGTGGTCAACCGG  
CGCGCCCCAGGTCGCTGAGGGACCCCGGCCAGGCGCGGAGATGGGG  
GTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCTGCTGTCG  
CTCCCTCTGGGCCTCCCAGTCCTGGGCGCCCCACCACGCCTCATCTGT  
GACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG  
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT  
ATCACTGTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGAT  
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG  
CTGTCGGAAGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCC  
CAGCCGTGGGAGCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG  
CCTTCGCAGCCTCACCCTCTGCTTCGGGCTCTGCGAGCCCAGAAGG  
AAGCCATCTCCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACA  
ATCACTGCTGACACTTTCCGCAAACTCTTCCGAGTCTACTCCAATTTC  
CTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG  
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC  
TCACCAACATTGCTTGTGCCACACCCTCCCCCGCCACTCCTGAACCCC  
GTCGAGGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA  
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC  
AACTCTGAGATCTAAGGATGTCACAGGGCCAACCTTGAGGGCCCAGAG  
CAGGAAGCATTGAGAGAGCAGCTTTAAACTCAGGGACAGAGCCATG  
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC  
AGGACACGCTTTGGAGGCGATTTACCTGTTTTTCGCACCTACCATCAGG  
GACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAG  
GTCTCACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA  
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCTCTGG  
CTCTCATGGGGTCCAAGTTTTGTGTATTCTTCAACCTCATTGACAAGA  
ACTGAAACCACCAAAAAAAAAAAAAA

288/497

FIG. 64B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu Leu Ser  
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser  
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr  
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys  
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val  
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu  
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser  
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile  
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe  
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr  
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

FIG. 65

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala  
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn  
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly  
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg  
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val  
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly  
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr  
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly  
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp

289/497

FIG. 66A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT  
CTCTGCACCCGCCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGC  
ATGTGAATGCCATCCAGGAGGCCCCGGCGTCTCCTGAACCTGAGTAGA  
GACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAT  
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGT  
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTG  
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA  
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA  
ACCTGAAGGACTTTCTGCTTGTTCATCCCCTTTGACTGCTGGGAGCCAG  
TCCAGGAGTGA

FIG. 66B

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro  
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu  
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr  
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg  
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro  
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser  
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu  
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu



290/497

FIG. 67A

ATGAAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTTG  
GGTTCTCTTGGCTGTTACTGCCAGGACCCATATGTAAAAGAAGCAGA  
AAACCTTAAGAAATATTTTAATGCAGGTCATTCAGATGTAGCGGATA  
ATGGAACCTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT  
GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACCT  
TTTTAAAACTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA  
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG  
AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT  
GAATGTCCAACGCAAAGCAATACATGAACTCATCCAAGTGATGGCTG  
AACTGTCCGCCAGCAGCTAAAACAGGGAAGCGAAAAAGGAGTCAGAT  
GCTGTTTCGAGGTCGAAGAGCATCCCAGTAA

FIG. 67B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu  
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr  
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile  
Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser  
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val  
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys  
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln  
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys  
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln

291/497

FIG. 68A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT  
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA  
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC  
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC  
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA  
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC  
CCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGA  
ATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTC  
CAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT  
GACCACCGGCAATGGCCTGTTCTCAGCGAGGGCCTGAAGCTAGTGG  
ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTC  
ACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACG  
ATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAG  
GAGCTTGACAGAGACACAGTTTTTGTCTCTGGTGAATTACATCTTCTTT  
AAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAG  
AGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATG  
AAGCGTTTAGGCATGTTTAAACATCCAGCACTGTAAGAAGCTGTCCAG  
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT  
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACC  
CACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGC  
CAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAA  
GAGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGG  
CTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTCTCCAAG  
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGC  
TGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCCCCCCCGA  
GGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATAC  
CAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAAT  
AACTGCCTCTCGCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCC  
CTGGATGACATTAAAGAAGGGTTGAGCTGG

292/497

FIG. 68B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val  
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser  
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe  
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe  
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp  
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala  
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln  
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val  
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val  
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys  
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val  
Phe Ala Leu Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val  
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser  
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro  
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys  
Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile  
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys  
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala  
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro  
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val  
Val Asn Pro Thr Gln Lys

293/497

FIG. 69A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTTT  
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCT  
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTCAAGTCCTTCCA  
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC  
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTTCGTGGGCATCAGGT  
GCCCCCCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGT  
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCCGACCTTTCCT  
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGGCGACG  
GATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGCACAG  
GCCTGCTACTGACCCTGCAGCCAGAACAGAAAGTTCCAGAAAGTGAAG  
GGATTTGGAGGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC  
CTGTCACCCCCTGCCCAAATTTGCTACTTAAATCGTACTTCTCTGAA  
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA  
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCCA  
GTTGCACAACTTCAGCCTCCCAGAGGAAGATACCAAGCTCAAGATAC  
CCCTGATTCACCGAGCCCTGCAGTTGGCCCAGCGTCCCGTTTCACTCC  
TTGCCAGCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG  
GTGAATGGGAAGGGGTCACTCAAGGGACAGCCCGGAGACATCTACC  
ACCAGACCTGGGCCAGATACTTTGTGAAGTTCCTGGATGCCTATGCTG  
AGCACAAGTTACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCT  
GCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGGGCTTCACCCCT  
GAACATCAGCGAGACTTCATTGCCCCGTGACCTAGGTCTACCCCTCGCC  
AACAGTACTCACCACAATGTCCGCCTACTCATGCTGGATGACCAACGC  
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC  
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCT  
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA  
ACACCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTTCTGGG  
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC  
CACAGCATCATCACGAACCTCCTGTACCATGTGGTTCGGCTGGACCGAC  
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA  
CTTTGTCGACAGTCCCATCATTGTAGACATCACCAAGGACACGTTTTA  
CAAACAGCCCATGTTCTACCACCTTGGCCACTTCAGCAAGTTCATTCC  
TGAGGGCTCCCAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC  
TGGACGCAGTGGCACTGATGCATCCCGATGGCTCTGCTGTTGTGGTCG  
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG  
CTGTGGGCTTCCTGGAGACAATCTCACCTGGCTACTCCATTACACCT  
ACCTGTGGCATCGCCAGTGATGGAGCAGATACTCAAGGAGGCACTGG  
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAGCTCACACGCTGTCTG  
TGACTAAAGAGGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

294/497

FIG. 69A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCCCTCTAGGTGGT  
GCCCAGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTC  
CCCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT  
TGGAAGCT

FIG. 69B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser  
Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser  
Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys  
Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr  
Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly  
Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln  
Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu  
Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser  
Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser  
Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser  
Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu  
Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys  
Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile  
Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu  
His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu  
Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp  
Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg  
Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val  
Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu  
Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro  
Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser  
Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn  
Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu  
Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr  
Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys  
Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu  
Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn  
Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu  
Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

295/497

FIG. 70A

ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG  
AGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCGATTTCAGAA  
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAACGCA  
GATGATATAACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA  
GCAACCGGGTGGAATATTGCTGGTGCAACAGTGGCAGGGCACAGTGC  
CACTCAGTGCCCTGTCAAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG  
GGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTCTGTGCCAGTG  
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATAACCAGGGCCA  
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGCACGTGGAGCAC  
AGCGGAGAGTGGCGCCGAGTGCACCAACTGGAACAGCAGCGCGTTG  
GCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG  
GCCTGGGGAACCACAACTACTGCAGAAACCCAGATCGAGACTCAA  
GCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCT  
GCAGCACCCCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGG  
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC  
CTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACAC  
AGCACAGAACCCAGTGCCAGGCACTGGGCCTGGGCAAACATAATT  
ACTGCCGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG  
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTC  
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG  
GAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCT  
TTGCCAAGCACAGGAGGTCGCCGGGAGAGCGGTTCTGTGCGGGGGC  
ATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCCTGCTTCCAG  
GAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATA  
CCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA  
TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACAT  
TGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCAGGAGA  
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTG  
CCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC  
CTTGTCTCCTTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTCAGACT  
GTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAG  
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCC  
CAGGCAAACCTTGACGACGCCTGCCAGGGCGATTTCGGGAGGCCCCCT  
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT  
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAG  
GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGACC  
AGGAACACCCGACTCCTCAAAAGCAAATGAGATCC

296/497

FIG. 70B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val  
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr  
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp  
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly  
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn  
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro  
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu  
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys  
Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp  
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp  
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser  
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr  
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met  
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu  
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His  
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser  
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe  
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser  
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser  
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly  
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys  
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu  
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg  
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu  
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys  
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn  
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro  
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly  
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg  
Asp Asn Met Arg Pro

297/497

FIG. 71A

ATCACTCTCTTTAATCACTACTCACATTAACCTCAACTCCTGCCACAA  
TGTACAGGATGCAACTCCTGTCTTGCAATTGCACTAATTCTTGCACTTG  
TCACAAACAGTGACCTACTTCAAGTTCGACAAAGAAAACAAAGAAA  
ACACAGCTACAACCTGGAGCATTTACTGCTGGATTTACAGATGATTTTG  
AATGGAATTAATAATTACAAGAATCCCAAACCTCACCAGGATGCTCAC  
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC  
AGTGTCTAGAAGAAGAAGTCAAACCTCTGGAGGAAGTGCTGAATTTA  
GCTCAAAGCAAAAACCTTTCACCTTAAGACCCAGGGACTTAATCAGCAA  
TATCAACGTAATAGTTCTGGAAGTAAAGGGATCTGAAACAACATTCA  
TGTGTGAATATGCAGATGAGACAGCAACCATTGTAGAATTTCTGAAC  
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAAGTTGATAA  
TTAAGTGCTTCCCCTTAAACATATCAGGCCTTCTATTTATTTATTTA  
AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG  
TAACTATTATTCTTAATCTTAAACTATAAATATGGATCTTTTATGAT  
TCTTTTTGTAAGCCCTAGGGGCTCTAAAATGGTTTACCTTATTTATCC  
CAAAAATATTTATTATTATGTTGAATGTTAAATATAGTATCTATGTAG  
ATTGGTTAGTAAACTATTTAATAAATTTGATAAATATAAAAAAAAAA  
AAACAAAAAAAAAAAA

FIG. 71B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn  
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu  
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn  
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr  
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val  
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser  
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu  
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys  
Gln Ser Ile Ile Ser Thr Leu Thr



FIG. 72A-1

298/497

ATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTGCATTCT  
GCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAAGTGTCA  
TGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG  
ATTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGT  
GTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTCAACAT  
CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCC  
AGGCTGAGGTTTATGATACAGTGGTCACTTAAAGAACATGGCT  
TCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCT  
TCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAG  
AAGATGATAAAGTCTTCCCTGGTGAAGCCATACATATGTCTGGCAG  
GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC  
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG  
CCTCATTGGAGCCCTACTAGTATGTAGAGAAGGGAGTCTGGCCAAGG  
AAAAGACACAGACCTTGCACAAATTTATACTACTTTTTGCTGTATTTG  
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATGCA  
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCTAAAATGCACACAG  
TCAATGGTTATGTAAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA  
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAA  
GTGCACTCAATATTCCTCGAAGGTCACACATTTCTTGTGAGGAACCAT  
CGCCAGGCGTCCTTGGAATCTCGCCAATAACTTTCTTACTGCTCAA  
ACACTCTTGATGGACCTTGGACAGTTTCTACTGTTTTGTCATATCTCT  
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT  
CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG  
ACTATGATGATGATCTTACTGATTCTGAAATGGATGTGGTCAGGTTTG  
ATGATGACAACTCTCCTTCCTTTATCCAAATTCGCTCAGTTGCCAAGA  
AGCATCCTAAAACTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC  
TGGGACTATGCTCCCTTAGTCCTCGCCCCCGATGACAGAAGTTATAAA  
AGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAA  
AAAAGTCCGATTTATGGCATAACAGATGAAACCTTTAAGACTCGTG  
AAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG  
AAGTTGGAGACACACTGTTGATTATTTAAGAATCAAGCAAGCAGA  
CCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTAT  
TCAAGGAGATTACCAAAGGTGTAAACATTTGAAGGATTTTCCAAT  
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGACTGTAGAAG  
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA  
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC  
TCCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGATA  
ATGTCAGACAAGAGGAATGTCATCCTGTTTTCTGTATTTGATGAGAAC  
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTTCTCCCAATCCA  
GCTGGAGTGCAGCTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT  
GCACAGCATCAATGGCTATGTTTTTGATAGTTTGCAGTTGTCAGTTTG  
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTGGAGCACAGA  
CTGACTTCCTTTCTGTCTTCTCTCTGGATATACCTTCAAACACAAAAT

## FIG. 72A-2

299/497

GGTCTATGAAGACACACTCACCTATTCCCATTTCTCAGGAGAACTGT  
CTTCATGTCGATGGAAAACCCAGGTCTATGGATTCTGGGGTGCCACA  
ACTCAGACTTTTCGGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT  
AGTTGTGACAAGAACAACACTGGTGATTATTACGAGGACAGTTATGAAGA  
TATTTTCAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCAAGAA  
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCCAAAAGCAATTT  
AATGCCACCACAATTCCAGAAAATGACATAGAGAAGACTGACCCTTG  
GTTTGACACACAGAACACCTATGCCTAAAATACAAAATGTCTCCTCTA  
GTGATTTGTTGATGCTCTTGCGACAGAGTCCTACTCCACATGGGCTAT  
CCTTATCTGATCTCCAAGAAGCCAAATATGAGACTTTTTCTGATGATC  
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA  
CACTTCAGGCCACAGCTCCATCACAGTGGGGACATGGTATTTACCCC  
TGAGTCAGGCCTCCAATTAAGATTAAATGAGAACTGGGGACAACCTG  
CAGCAACAGAGTTGAAGAACTTGATTTCAAAGTTTCTAGTACATCA  
AATAATCTGATTTCAACAATTCCATCAGACAATTTGGCAGCAGGTACT  
GATAATACAAGTTCCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT  
AGTCAATTAGATAACCACTCTATTTGGCAAAAAGTCATCTCCCCTTACT  
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAATAATGATTCAA  
GTTGTTAGAATCAGGTTTAATGAATAGCCAAGAAAGTTCATGGGGAA  
AAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGGAAAAGA  
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAGTT  
AGCATCTCTTTGTTAAAGACAAAACAACTTCCAATAATTCAGCAACT  
AATAGAAAGACTCACATTGATGGCCCATCATTATTAATTGAGAATAG  
TCCATCAGTCTGGCAAAATATATTAGAAAGTGACACTGAGTTTAAAA  
AAGTGACACCTTTGATTCATGACAGAATGCTTATGGACAAAAATGCT  
ACAGCTTTGAGGCTAAATCATATGTCAAATAAACTACTTCATCAA  
AAACATGGAAATGGTCCAACAGAAAAAAGAGGGGCCCATTCACCA  
GATGCACAAAATCCAGATATGTGCTTCTTTAAGATGCTATTCTTGCCA  
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA  
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCCTTAGGACCAG  
AAAAATCTGTGGAAGGTCAGAAATTTCTTGTCTGAGAAAAACAAAGTG  
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA  
TGGTTTTTCCAAGCAGCAGAAACCTATTTCTTACTAACTTGGATAATT  
TACATGAAAATAATACACACAATCAAGAAAAAAAATTTCAGGAAGA  
AATAGAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTTGCCTC  
AGATACATACAGTGACTGGCACTAAGAATTTTCATGAAGAACCTTTTC  
TACTGAGCACTAGGCCAAAATGTAGAAGGTTTCATATGACGGGGCATA  
TGCTCCAGTACTTCAAGATTTTAGGTCATTAAATGATTCAACAAATAG  
AACAAAGAAACACACAGCTCATTCTCAAAAAAAGGGGAGGAAGAA  
AACTTGGAAGGCTTGGGAAATCAAACCAGCAAATTGTAGAGAAATAT  
GCATGCACCACAAGGAATATCTCCTAATAACAAGCCAGCAGAAATTTG  
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCCTA

FIG. 72A-3

300/497

GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC  
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCCCTCACAC  
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC  
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAATAGA  
TCTCCATTACCCATTGCAAAGGTATCATCATTTCCATCTATTAGACCTA  
TATATCTGACCAGGGTCCTATTCCAAGACAACCTCTTCTCATCTTCCAG  
CAGCATCTTATAGAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT  
TTCTTACAAGGAGCCAAAAAAATAACCTTTCTTTAGCCATTCTAACC  
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG  
TGCCACAAATTCAGTCACATACAAGAAAGTTGAGAACACTGTTCTCCC  
GAAACCAGACTTGCCCAAAACATCTGGCAAAGTTGAATTGCTTCCAA  
AAGTTCACATTTATCAGAAGGACCTATTCCCTACGGAACTAGCAATG  
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA  
CAGAGGGAGCGATTAAGTGGAATGAAGCAAACAGACCTGGAAAAGT  
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAAGACTCCCTCCAA  
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC  
AAAAGAAGAGTGGAAATCCCAAGAGAAGTCACCAGAAAAAACAGCT  
TTTAAGAAAAAGGATACCATTTTGTCCCTGAACGCTTGTGAAAGCAAT  
CATGCAATAGCAGCAATAAATGAGGGACAAAATAAGCCCGAAATAG  
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA  
AACCACCAAGTCTTGAAACGCCATCAACGGGAAATAACTCGTACTAC  
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT  
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAATC  
AGAGCCCCCGCAGCTTTCAAAGAAAACACGACACTATTTTATTGCTG  
CAGTGGAGAGGGCTCTGGGATTATGGGATGAGTAGCTCCCCACATGTT  
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAAGAAAGT  
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT  
GGAGAACTAAATGAACATTTGGGACTCCTGGGGCCATATATAAGAGC  
AGAAGTTGAAGATAATATCATGGTAACTTTCAGAAATCAGGCCTCTC  
GTCCCTATTCTTCTATTCTAGCCTTATTTCTTATGAGGAAGATCAGAG  
GCAAGGAGCAGAACCTAGAAAAAACTTTGTCAAGCCTAATGAAACCA  
AACTTACTTTTGGAAGGTGCAACATCATATGGCACCCACTAAAGAT  
GAGTTTGAAGTGCAGAGCCTGGGCTTATTTCTCTGATGTTGACCTGGAA  
AAAGATGTGCACTCAGGCCTGATTGGACCCCTTCTGGTCTGCCACACT  
AACACACTGAACCCTGCTCATGGGAGACAAGTGACAGTACAGGAATT  
TGCTCTGTTTTTACCATCTTTGATGAGACCAAAGCTGGTACTTCACT  
GAAAATATGGAAAGAACTGCAGGGCTCCCTGCAATATCCAGATGGA  
AGATCCCCTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA  
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA  
TTCGATGGTATCTGCTCAGCATGGGCAGCAATGAAAACATCCATTCT  
ATTCATTTAGTGGACATGTGTTCACTGTACGAAAAAAAGAGGAGTA  
TAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGAGACAGTGA

FIG. 72A-4

301/497

AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGGGAATGCCTTATTGG  
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA  
TAAGTGTGAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT  
TCAGATTACAGCTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG  
CCAGACTTCATTATTCCGGATCAATCAATGCCTGGAGCACCAAGGAG  
CCCTTTTCTTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTAC  
GGCATCAAGACCCAGGGTGGCCGTCAGAAGTTCTCCAGCCTCTACAT  
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA  
CTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATG  
TGGATTTCATCTGGGATAAAACACAATATTTTAAACCCTCCAATTATTG  
CTCGATACATCCGTTTGCACCCAACCTCATTATAGCATTTCGAGCACTC  
TTCGCATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCAT  
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA  
TCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAGCTCGA  
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA  
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA  
CAGGAGTAACTACTCAGGGAGTAAATCTCTGCTTACCAGCATGTAT  
GTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC  
TCTCTTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGA  
CTCCTTCACACCTGTGGTGAACCTCTAGACCCACCGTACTGACTCG  
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAG  
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC  
CACTGCAGCACCTGCCACTGCCGTACCTCTCCCTCCTCAGCTCCAGG  
GCAGTGTCCCTCCCTGGCTTGCCTTCTACCTTTGTGCTAAATCCTAGC  
AGACACTGCCTTGAAGCCTCCTGAATTAACCTATCATCAGTCCTGCATT  
TCTTTGGTGGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACCTCTTA  
CCTATTTTCTGCAGCTGCTCCCAGATTACTCCTTCCTTCCAATATAACT  
AGGCAAAAAGAAGTGAGGAGAAACCTGCATGAAAGCATTCTTCCCTG  
AAAAGTTAGGCCTCTCAGAGTCACCACTTCCTCTGTTGTAGAAAACT  
ATGTGATGAAACTTTGAAAAAGATATTTATGATGTTAACATTTACAGGT  
TAAGCCTCATACGTTTAAAATAAACTCTCAGTTGTTTATTATCCTGA  
TCAAGCATGGAACAAAGCATGTTTCAGGATCAGATCAATACAATCTT  
GGAGTCAAAGGCAAATCATTGGACAATCTGCAAAATGGAGAGAA  
TACAATACTACTACAGTAAAGTCTGTTTCTGCTTCCTTACACATAGA  
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCAA  
AACTAGCATTCTTAACTGAGAATTATAGATGGGGTTCAAGAATCCC  
TAAGTCCCCTGAAATTATATAAGGCATTCTGTATAAATGCAAATGTGC  
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT  
GACCAATAAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG  
AAATAAAATAACAATGTCTTCTTGAAATTTGTGATGGCCAAGAAAGA  
AAATGATGA

## FIG. 72B-1

302/497

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser  
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser  
Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe  
Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His  
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile  
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro  
Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr  
Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly  
Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro  
Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn  
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys  
Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser  
Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg  
Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu  
Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro  
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln  
Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp  
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu  
Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn  
Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val  
Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys  
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr  
Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn  
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr  
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro  
Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser  
Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg  
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile  
Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg  
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser  
Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn  
Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg  
Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln  
Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val  
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu  
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys  
His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val  
Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe

303/497

FIG. 72B-2

Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr  
Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn  
Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln  
Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp  
Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu  
Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu  
Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn  
Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val  
Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr  
Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu  
Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu  
Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly  
Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn  
Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly  
Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly  
Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu  
Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp  
Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser  
Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp  
Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser  
Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala  
Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg  
Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro  
Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu  
Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly  
Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp  
Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile  
Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr  
Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln  
Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg  
Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys  
Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val  
Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe  
Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu  
Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn  
Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu  
Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile  
Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile  
Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro

FIG. 72B-3

304/497

Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu  
Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr  
Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr  
Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser  
Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro  
Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu  
Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys  
Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu  
Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu  
Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile  
Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly  
Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg  
Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg  
Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu  
Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg  
Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp  
Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val  
Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro  
Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg  
Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro  
Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu  
Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val  
Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr  
Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu  
Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln  
Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu  
Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr  
Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro  
Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly  
Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys  
Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr  
Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu  
His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr  
Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln  
Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala  
Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile  
Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser  
Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly  
Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile

FIG. 72B-4

305/497

Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr  
His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn  
Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr  
Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu  
His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu  
Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln  
Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser  
Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe  
Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu  
Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg  
Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr



306/497

FIG. 73A

TCCACCTGTCCCCGCAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC  
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG  
GCGCGCCTGCTTCTCTGCGTCCTGGTCGTGAGCGACTCCAAAGGCAGC  
AATGAACTTCATCAAGTTCCATCGAACTGTGACTGTCTAAATGGAGGA  
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC  
CCAAAGAAATTTCGGAGGGGCAGCACTGTGAAATAGATAAGTCAAAAAC  
CTGCTATGAGGGGAATGGTCACTTTTACCGAGGAAAGGCCAGCACTG  
ACACCATGGGCGCGCCCTGCCTGCCCTGGAACCTTGCCACTGTCCTTC  
AGCAAACGTACCATGCCCACAGATCTGATGCTCTTCAGCTGGGCCTGG  
GGAAACATAATTACTGCAGGAACCCAGACAACCGGAGGCGACCCCTGG  
TGCTATGTGCAGGTGGGCCTAAAGCCGCTTGTCCAAGAGTGCATGGT  
GCATGACTGCGCAGATGGAAAAAAGCCCTCCTCTCCTCCAGAAGAAT  
TAAAATTTCAGTGTGGCCAAAAGACTCTGAGGCCCCCGCTTTAAGATTA  
TTGGGGGAGAATTCACCACCATCGAGAACCAGCCCTGGTTTGCGGCC  
ATCTACAGGAGGCACCGGGGGGGCTCTGTACCTACGTGTGTGGAGG  
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT  
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTGCTCAA  
GGCTTAACTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGAAAAC  
CTCATCCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC  
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA  
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA  
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA  
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA  
AGCTGATTTCCACCGGGAGTGTCAGCAGCCCCACTACTACGGCTCTG  
AAGTCACCACCAAAAATGCTGTGTGCTGCTGACCCACAGTGGAACA  
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA  
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC  
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC  
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA  
GGGTCCCCAGGGAGGAAACGGGCACCAACCCGCTTTCTTGCTGGTTGTC  
ATTTTTCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA  
AGAT

307/497

FIG. 73B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser  
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly  
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys  
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn  
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro  
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg  
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His  
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys  
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile  
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr  
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys  
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu  
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys  
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg  
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro  
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys  
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys  
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr  
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp  
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val  
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser  
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

308/497

FIG. 74A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA  
TAGACTACTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAATTGTCATCA  
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC  
ACCATCATCTCAGGATGAGGGGCGATGAAGCTGCTGGGGGCGCTGCTG  
GCACTGGCGGGCCCTACTGCAGGGGGGCCGTGTCCCTGAAGATCGCAGC  
CTTCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCT  
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT  
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG  
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT  
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTTCGTGTA  
CAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG  
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT  
GTCAGGTTCTTCTCCCGGTTACAGAGGTCAGGGAGTTTGCCATTGTT  
CCCCTGCATGCGGCCCCGGGGGACGCAGTAGCCGAGATCGACGCTCT  
CTATGACGTCTACCTGGATGTCCAAGAGAAATGGGGCTTGGAGGACG  
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT  
CCCAGTGGTCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGC  
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT  
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGCGCCGTTGTTT  
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG  
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG  
CTGAAGTGAGCAGCCCCTCCCCACACCAGTTGAACTGCAG

309/497

FIG. 74B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu Leu Gln  
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys  
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile  
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu  
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro  
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln  
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile  
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp  
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln  
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser  
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln  
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
Glu Val Met Leu Lys

310/497

FIG. 75A

GCTGCATCAGAAGAGGCCATCAAGCACATCACTGTCCTTCTGCCATGG  
CCCTGTGGATGCGCCTCCTGCCCCTGCTGGCGCTGCTGGCCCTCTGGG  
GACCTGACCCAGCCGCAGCCTTTGTGAACCAACACCTGTGCGGCTCAC  
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT  
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA  
GGTGGAGCTGGGCGGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG  
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT  
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG  
CAGCCCGCAGGCAGCCCCCACC CGCCCTCCTGCACCGAGAGAGA  
TGGAATAAAGCCCTTGAACCAGC

FIG. 75B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly  
Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val  
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr  
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro  
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile  
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

311/497

FIG. 76A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT  
TTCTGTTCCCAATCCTCTGGGATTCTTTCCCGATCACCAGTTGGACCCT  
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA  
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC  
GGGCCAGGGTTCACCCCAACACACGGCGGTCTTTTGGGGTGGAGCCC  
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCCTG  
TTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC  
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAAGTCCACAACA  
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGGCCTATATTTTCT  
GCTGGTGGCTCCAGTTCCGGAACAGTAAACCCTGTTCCGACTACTGTC  
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCTGCACCGAAC  
ATGGAGAGCACAACATCAGGATTCTAGGACCCCTGCTCGTGTTACA  
GGCGGGGTTTTTCTTGTTGACAAGAATCCTCACAATACCACAGAGTCT  
AGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGGAGCACCCACGTG  
TCCTGGCCAAAATTTCGCAGTCCCCAACCTCCAATCACTCACCAACCTC  
TTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTTT  
ATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTC  
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA  
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCTGCT  
CAAGGAACCTCTATGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC  
GGAAACTGCACCTTGTAATCCCATCCCATCATCCTGGGCTTTCGCAAGA  
TTCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA  
GTGCCATTTGTTCAAGTGGTTCGCAGGGCTTTCCCCCACTGTTTGGCTTT  
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT  
TGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATAC  
ATTTGA

312/497

FIG. 76B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro  
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn  
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile  
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu  
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro  
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg  
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu  
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val  
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp  
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu  
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser  
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser  
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr  
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu  
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu  
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala  
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn  
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp  
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala  
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro  
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu  
Trp Val Tyr Ile

313/497

FIG. 77A

CGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA  
CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGC  
CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGC  
CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT  
TTGACACCTACCAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG  
AAGTATTCATTCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG  
TCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAA  
CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA  
GCCCCGTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG  
CGCCTCTGACAGCAACGTCTATGACCTCCTAAAGGACCTAGAGGAAG  
GCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGGACT  
GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACA  
CAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG  
GAAGGACATGGCAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCG  
CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG  
TGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGT  
GCCCAACAGCCTTGTCTAATAAAATTAAGTTGCATC

FIG. 77B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu  
Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp  
Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln  
Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro  
Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr  
Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp  
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala  
Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly  
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile  
Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe



314/497

FIG. 78A

ATGTATTCCAATGTGATAGGAACTGTAACCTCTGGAAAAAGGAAGGT  
TTATCTTTTGTCTTGCTGCTCATTGGCTTCTGGGACTGCGTGACCTGT  
CACGGGAGCCCTGTGGACATCTGCACAGCCAAGCCGCGGGACATTCC  
CATGAATCCCATGTGCATTTACCGCTCCCCGGAGAAGAAGGCAACTG  
AGGATGAGGGCTCAGAACAGAAGATCCCGGAGGCCACCAACCGGCG  
TGTCTGGGAACTGTCCAAGGCCAATTCCCGCTTTGCTACCACTTTCTA  
TCAGCACCTGGCAGATTCCAAGAATGACAATGATAACATTTTCCTGTC  
ACCCCTGAGTATCTCCACGGCTTTTGCTATGACCAAGCTGGGTGCCTG  
TAATGACACCCTCCAGCAACTGATGGAGGTATTTAAGTTTGACACCAT  
ATCTGAGAAAACATCTGATCAGATCCACTTCTTCTTTGCCAAACTGAA  
CTGCCGACTCTATCGAAAAGCCAACAAATCCTCCAAGTTAGTATCAGC  
CAATCGCCTTTTTTGAGACAAATCCCTTACCTTCAATGAGACCTACCA  
GGACATCAGTGAGTTGGTATATGGAGCCAAGCTCCAGCCCCCTGGACT  
TCAAGGAAAATGCAGAGCAATCCAGAGCGGCCATCAACAAATGGGTG  
TCCAATAAGACCGAAGGCCGAATCACCGATGTCATTCCCTCGGAAGC  
CATCAATGAGCTCACTGTTCTGGTGCTGGTTAACACCATTACTTCAA  
GGGCCTGTGGAAGTCAAAGTTCAGCCCTGAGAACACAAGGAAGGAAC  
TGTTCTACAAGGCTGATGGAGAGTCGTGTTTCAGCATCTATGATGTACC  
AGGAAGGCAAGTTCCGTTATCGGCGCGTGGCTGAAGGCACCCAGGTG  
CTTGAGTTGCCCTTCAAAGGTGATGACATCACCATGGTCCTCATCTTG  
CCCAAGCCTGAGAAGAGCCTGGCCAAGGTGGAGAAGGAACACCCC  
AGAGGTGCTGCAGGAGTGGCTGGATGAATTGGAGGAGATGATGCTGG  
TGGTCCACATGCCCCGCTTCCGCATTGAGGACGGCTTCAGTTTGAAGG  
AGCAGCTGCAAGACATGGGCCTTGTCGATCTGTTCAGCCCTGAAAAG  
TCCAAACTCCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTC  
TCAGATGCATTCCATAAGGCATTTCTTGAGGTAAATGAAGAAGGCAG  
TGAAGCAGCTGCAAGTACCGCTGTTGTGATTGCTGGCCGTTTCGCTAAA  
CCCCAACAGGGTGACTTTCAAGGCCAACAGGCCTTTCCTGGTTTTTAT  
AAGAGAAGTTCCTCTGAACACTATTATCTTCATGGGCAGAGTAGCCA  
ACCCTTGTGTTAAGTAA

315/497

FIG. 78B

Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val Tyr Leu Leu  
Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys His Gly Ser Pro Val Asp  
Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn Pro Met Cys Ile Tyr Arg Ser  
Pro Glu Lys Lys Ala Thr Glu Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr  
Asn Arg Arg Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr  
Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser  
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr Leu Gln Gln  
Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Ile His  
Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser  
Lys Leu Val Ser Ala Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu  
Thr Tyr Gln Asp Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe  
Lys Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr  
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu Thr Val Leu  
Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Ser Pro Glu  
Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser  
Met Met Tyr Gln Glu Gly Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln  
Val Leu Glu Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys  
Pro Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu  
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg Phe Arg  
Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met Gly Leu Val Asp  
Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile Val Ala Glu Gly Arg Asp Asp  
Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser  
Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg  
Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn  
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys

316/497

FIG. 79A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG  
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCAG  
AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCA  
ATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCCA  
CTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAGA  
GTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCAAGTAATGGG  
GGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTT  
ATTATCACAAATCTTAA

FIG. 79B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu  
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu  
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe  
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn  
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met  
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His  
Lys Ser

317/497

FIG. 79C

ATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC  
GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCAT  
CAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCA  
CCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCG  
TGCTGCAGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACC  
GCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCGCGCGGGCG  
TGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCAC  
TCTGCCGCCGCAGCACTGACTGCGGGGGTCCCAAGGACCACCCC  
TTGACCTGTGATGACCCCGCTTCCAGGACTCCTCTTCTCAAAGGCC  
CCTCCCCCAGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGAC  
ACCCCGATCCTCC CACAATAA

FIG. 79D

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr  
Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala  
Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly  
Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val  
Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg  
Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys  
Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp  
Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser  
Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln

FIG. 80A

318/497

ATGCGTCCCCTGCGCCCCCGCGCCGCGCTGCTGGCGCTCCTGGCCTCG  
CTCCTGGCCGCGCCCCCGGTGGCCCCGGCCGAGGCCCGCACCTGGT  
GCAGGTGGACGCGGCCCGCGCGCTGTGGCCCCTGCGGCGCTTCTGGA  
GGAGCACAGGCTTCTGCCCCCGCTGCCACACAGCCAGGCTGACCAG  
TACGTCTCAGCTGGGACCAGCAGCTCAACCTCGCCTATGTGGGCGCC  
GTCCCTCACCGCGGCATCAAGCAGGTCCGGACCCACTGGCTGCTGGA  
GCTTGTACCAACCAGGGGGTCCACTGGACGGGGCCTGAGCTACAAC  
TCACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCC  
TCCAGGGTTTGAGCTGATGGGCAGCGCCTCGGGCCACTTCACTGACT  
TTGAGGACAAGCAGCAGGTGTTTGAGTGGAAGGACTTGGTCTCCAGC  
CTGGCCAGGAGATACATCGGTAGGTACGGACTGGCGCATGTTTCCAA  
GTGGAACCTTCGAGACGTGGAATGAGCCAGACACCACGACTTTGACA  
ACGTCTCCATGACCATGCAAGGCTTCCTGAACACTACGATGCCTGCT  
CGGAGGGTCTGCGCGCCGCCAGCCCCGCCCTGCGGCTGGGAGGCCCC  
GGCGACTCCTTCCACACCCACCGCGATCCCCGCTGAGCTGGGGCCTC  
CTGCGCCACTGCCACGACGGTACCAACTTCTTCACTGGGGAGGCGGG  
CGTGCGGCTGGACTACATCTCCCTCCACAGGAAGGGTGCGCGCAGCT  
CCATCTCCATCCTGGAGCAGGAGAAGGTCGTCGCGCAGCAGATCCGG  
CAGCTCTTCCCCAAGTTCGCGGACACCCCCATTTACAACGACGAGGCG  
GACCCGCTGGTGGGCTGGTCCCTGCCACAGCCGTGGAGGGCGGACGT  
GACCTACGCGGCCATGGTGGTGAAGGTCATCGCGCAGCATCAGAACC  
TGCTACTGGCCAACACCACCTCCGCCTTCCCCTACGCGCTCCTGAGCA  
ACGACAATGCCTTCCTGAGCTACCACCCGCACCCCTTCGCGCAGCGCA  
CGCTACCCGCGCGCTTCCAGGTCAACAACACCCGCCCGCCGCACGTG  
CAGCTGTTGCGCAAGCCGGTGCTCACGGCCATGGGGCTGCTGGCGCT  
GCTGGATGAGGAGCAGCTCTGGGCCGAAGTGTCGCAGGCCGGGACCG  
TCCTGGACAGCAACCACACGGTGGGCGTCCTGGCCAGCGCCCACCGC  
CCCCAGGGCCCCGGCCGACGCCTGGCGCGCCGCGGTGCTGATCTACGC  
GAGCGACGACACCCGCGCCCAACCCAAACCGCAGCGTCGCGGTGACCC  
TGCGGCTGCGCGGGGTGCCCCCGGCCCGGGCCTGGTCTACGTCACG  
CGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGGCGGCG  
CCTGGGCCGGCCCGTCTTCCCCACGGCAGAGCAGTTCCGGCGCATGC  
GCGCGGCTGAGGACCCGGTGGCCGCGGCGCCCCGCCCTTACCCGCC  
GGCGGCCGCTGACCCTGCGCCCCGCGCTGCGGCTGCCGTCGCTTTTG  
CTGGTGCACGTGTGTGCGCGCCCCGAGAAGCCGCCCGGGCAGGTCAC  
GCGGCTCCGCGCCCTGCCCCCTGACCCAAGGGCAGCTGGTTCTGGTCTG  
GTCGGATGAACACGTGGGCTCCAAGTGCCTGTGGACATACGAGATCC  
AGTTCTCTCAGGACGGTAAGGCGTACACCCCGGTACGACAGGAAGCCA  
TCGACCTTCAACCTCTTTGTGTTTCAGCCCAGACACAGGTGCTGTCTCT  
GGCTCCTACCGAGTTCGAGCCCTGGACTACTGGGCCCCGACCAGGCCC  
CTTCTCGGACCCTGTGCCGTACCTGGAGGTCCCTGTGCCAAGAGGGCC  
CCCATCCCCGGGCAATCCATGA

319/497

FIG. 80B

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu  
Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val Gln Val Asp Ala Ala  
Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu  
Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala  
Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu  
Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His  
Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu  
Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val  
Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly  
Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His Asp  
Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys  
Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser  
Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp  
Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His  
Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln  
Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala  
Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala  
Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr  
Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro  
His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg  
Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala  
Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu  
Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala  
Asp Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro  
Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu  
Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp  
Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg  
Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu  
Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala  
Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln  
Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr  
Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro  
Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr  
Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro  
Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro

320/497

FIG. 81A

ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCGCT  
TCGCTTCCTGGCCCTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACT  
GGACAATGGATTGGCAAGGACGCCTACCATGGGCTGGCTGCACTGGG  
AGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCAGATTCCTGC  
ATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGA  
AGGCTGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTG  
GATGGCTCCCCAAAGAGATTCAGAAGGCAGACTTCAGGCAGACCCTC  
AGCGCTTTCCTCATGGGATTCGCCAGCTAGCTAATTATGTTACAGCA  
AAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAAACCTGC  
GCAGGCTTCCCTGGGAGTTTTGGATACTACGACATTGATGCCCAGACC  
TTTGCTGACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGT  
GACAGTTTGGAAAATTTGGCAGATGGTTATAAGCACATGTCCTTGGCC  
CTGAATAGGACTGGCAGAAGCATTGTGTACTCCTGTGAGTGGCCTCTT  
TATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGACAGTAC  
TGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAGT  
ATAAAGAGTATCTTGGAAGTGGACATCTTTTAACCAGGAGAGAATTGTT  
GATGTTGCTGGACCAGGGGGTTGGAATGACCCAGATATGTTAGTGAT  
TGGCAACTTTGGCCTCAGCTGGAATCAGCAAGTAACTCAGATGGCCCT  
CTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTCCGACA  
CATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGC  
CATCAATCAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGG  
GAGACAACCTTTGAAGTGTGGGAACGACCTCTCTCAGGCTTAGCCTGG  
GCTGTAGCTATGATAAACCGGCAGGAGATTGGTGGACCTCGCTCTTAT  
ACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCTGCC  
TGCTTCATCACACAGCTCCTCCCTGTGAAAAGGAAGCTAGGGTTCTAT  
GAATGGACTTCAAGGTAAAGAAGTCACATAAATCCCACAGGCACTGT  
TTTGCTTCAGCTAGAAAATACAATGCAGATGTCATTAAAAGACTTACT  
TTAA

321/497

FIG. 81B

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe  
Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly Leu Ala  
Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met Cys Asn Leu Asp  
Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys Leu Phe Met Glu Met Ala Glu  
Leu Met Val Ser Glu Gly Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp  
Cys Trp Met Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln  
Arg Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys  
Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly Ser Phe  
Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly Val Asp Leu Leu Lys  
Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn Leu Ala Asp Gly Tyr Lys His  
Met Ser Leu Ala Leu Asn Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro  
Leu Tyr Met Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn  
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu  
Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro Gly Gly Trp  
Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu Ser Trp Asn Gln Gln  
Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp  
Leu Arg His Ile Ser Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala  
Ile Asn Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn  
Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser Leu Gly Lys  
Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu Leu Pro Val Lys Arg Lys  
Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr  
Val Leu Leu Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu



322/497

FIG. 82A

ATGGCGCCCGTCGCCGTCTGGGCGCGCTGGCCGTCGGACTGGAGCT  
CTGGGCTGCGGCGCACGCCTTGCCCGCCCAGGTGGCATTACACCTA  
CGCCCCGGAGCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC  
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA  
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG  
GACAGCACATACACCCAGCTCTGGAAGTGGGTTCCTGAGTGTGAG  
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAACTCAAGCCTGCAC  
TCGGGAACAGAACC GCATCTGCACCTGCAGGCCCGGCTGGTACTGCG  
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAG  
TGCCGCCCCGGGCTTCGGCGTGGCCAGACCAGGAAGTGAACATCAGA  
CGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCAACACGACTTC  
ATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACTGGTGGCCAT  
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA  
CCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCAGCCAGTGTCC  
ACACGATCCCAACACACGCAGCCAACTCCAGAAGCCAGCACTGCTCC  
AAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG  
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC  
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTCATCATGAC  
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC  
CTCACTTGCCCTGCCGATAAGGCCCGGGGTACACAGGGCCCCGAGCAG  
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA  
GAGCTCGGCCAGTGCCTTGGACAGAAGGGCGCCCACTCGGAACCAGC  
CACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGC  
CAGCACCGGGAGCTCAGATTCTTCCCCTGGTGGCCATGGGACCCAGG  
TCAATGTACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT  
CACAGTGCTCCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC  
AGCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCCTTCTCCAAGGA  
GGAATGTGCCTTTCGGTACAGCTGGAGACGCCAGAGACCCTGCTGG  
GGAGCACCGAAGAGAAGCCCCTGCCCTTGGAGTGCCTGATGCTGGG  
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTCTAGCCAAGG  
TGGGCTGAGCCCTGGCAGGATGACCCTGCGAAGGGGCCCTGGTCCTT  
CCAGGC

323/497

FIG. 82B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala  
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser  
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys  
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys  
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys  
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln  
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val  
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr  
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val  
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr  
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln  
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro  
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly  
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val  
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro  
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu  
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg  
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly  
Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln  
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys  
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro  
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu  
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro  
Asp Ala Gly Met Lys Pro Ser

324/497

FIG. 83A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro  
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

FIG. 83B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg  
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg  
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr  
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys  
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln  
Gly Thr Leu Val Thr Val Ser Ser

325/497

FIG. 84A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr  
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp  
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp  
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser  
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr  
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly  
Thr Thr Val Thr Val Ser Ser

FIG. 84B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys  
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser  
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe  
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys